

Supplemental Material: Materials and Methods

Cell culture and chemical treatments

Mouse Hepa-1c1c7 (Hepa-1) cells (Bernhard et al., 1973), and its mutant derivative *c35*, expressing a DNA-binding defective AHR (Sun et al., 1997) were grown in α -minimal essential medium supplemented with 5% (v/v) fetal bovine serum, 26 mM NaHCO₃ and 1 % (v/v) antibiotic-antimycotic mixture at 37°C in humidified 5% CO₂ atmosphere. When the cells reached 70-80% confluence they were treated with 5 μ M BaP, 5 nM TCDD, or 0.1% DMSO vehicle. Cells were then harvested 1.5 h and 8 h post-treatment for chromatin immunoprecipitation and RNA extraction, respectively. The phenotype of the *c35* cell line was verified (Marlowe et al., 2004) prior to use.

Chromatin immunoprecipitation

ChIP was performed with minor modifications of published procedures (Wells and Farnham, 2002) as modified in our laboratory (Schnekenburger et al., 2007b). Biological replicates of approximately 1.5 – 2 \times 10⁷ Hepa-1 cells were incubated for 10 min at room temperature with 1% formaldehyde. After cross-linking, the reaction was quenched with 0.125 M glycine for 10 min at room temperature. After rinsing twice with ice-cold 1X PBS, cells were scraped from the dishes, pelleted by centrifugation, resuspended in cell lysis buffer (5 mM PIPES [pH 8.0], 85 mM KCl, 0.5% NP-40, plus 1X protease inhibitor cocktail (Roche) and incubated on ice for 10 min. The nuclei were pelleted, resuspended in nuclei lysis buffer (50 mM Tris-HCl [pH 8.1], 10 mM EDTA, 1% SDS plus protease inhibitor cocktail) and incubated on ice for 10 min. Chromatin was sheared to a size range of 0.3 - 0.8 kb by sonication in a crushed-ice/water bath with six 30-sec bursts of 200 W with a 30-sec interval between bursts using a Bioruptor (Diagenode). After centrifugation to remove cell debris, chromatin was precleared for 1.5 h at 4°C with a 50% gel slurry of protein A-agarose beads saturated with salmon sperm DNA

and BSA (Upstate). The precleared chromatin was diluted 3 times in IP dilution buffer (16.7 mM Tris-Cl [pH 8.1], 167 mM NaCl, 1.2 mM EDTA, 1.1 % Triton X-100, 0.01% SDS), and 10% of the supernatants were used as inputs. The diluted chromatin was incubated overnight on a rotating platform at 4°C with the appropriate antibodies. The immune-complexes were recovered by a 2-hour incubation at 4°C with a 50% gel slurry of either protein A-agarose or protein-G-agarose beads (Upstate) depending on the antibody specificity. The agarose beads were pelleted and washed twice with 1X dialysis buffer (50 mM Tris-HCl [pH 8.0], 2 mM EDTA, 0.2% sarkosyl) and sequentially 4 times with IP wash buffer (100 mM Tris-HCl [pH 9.0], 500mM LiCl, 1% NP-40, 1% deoxycholic acid). Precipitated chromatin complexes were removed from the beads by incubation with elution buffer (50 mM NaHCO₃, 1% SDS), with mild vortexing. This step was repeated and the eluates were combined. All buffers were supplemented with 1X protease inhibitor cocktail (Complete minus EDTA, Roche). Cross-linking was reversed by adding NaCl to a final concentration of 0.3 M and incubated overnight at 65°C in the presence of RNase A. Samples were then digested with proteinase K at 45°C for 1.5 h. DNA was purified by chromatography on QIAquick® columns (Qiagen), eluted in ddH₂O, and an aliquot was used for analysis by PCR. The end-point PCR products were separated by electrophoresis through 15% polyacrylamide gels and visualized after staining with ethidium bromide. Immunoprecipitation was performed with ChIP-verified anti-AHR antibody (Biomol) or with control non-immune rabbit IgG (Upstate). An aliquot of immunoprecipitated purified DNA was checked for IP efficiency by real-time PCR using primers specific for the mouse *Cyp1a1* promoter domains known to be bound or not by AHR. A significant enrichment (16- to 32-fold) for the specific AHR target was observed relative to the control antibody.

Target Preparation

Immunoprecipitated DNA was PCR amplified and labeled according to the standard protocol supplied by Affymetrix (Affymetrix® Chromatin Immunoprecipitation Assay, (http://www.affymetrix.com/products/arrays/specific/mouse_promoter.affx) Protocol. Briefly, in a first step, anti-AHR or non-immune IgG immunoprecipitated DNA samples were linearly amplified, Samples were randomly primed at 95°C for 4 min with 40 µM of HPLC purified primer A: GTTTCCCAGTCACGGTC(N)₉ and then amplified in a reaction mixture composed of 75 µg/ml BSA, 5 µM DTT, 0.6 mM dNTPs and 1.3 U sequenase™ (USB) at 10°C for 5 min, ramped from 10°C to 37°C over 9 min, followed by 37°C for 8 min, 95°C for 4 min, snapped cold on ice, held at 10°C, and then adding 1.3 U of Sequenase™ and repeating the same cycle 2 more times. Linearly amplified DNA was purified with a Microspin S-300 HR columns (GE Healthcare) and the purified DNA was then PCR amplified in the following mix: 10 U Taq Polymerase (Qiagen), 0.75 mM MgCl₂, 4 µM of primer B (5'-GTTTCCCAGTCACGGTC-3'), 375 µM of dNTPs/dUTP mix, 1X of PCR buffer. Cycling conditions were: 95°C for 30 s, 45°C for 30 s, 55°C for 30 s, 72°C for 1 min for 15 cycles followed by 15 additional cycles of 95°C for 30 s, 45°C for 30 s, 55°C for 30 s and 72°C for 1 min. Amplified DNA was purified with a Minelute PCR purification kit (Qiagen) and eluted twice with 20 µl ddH₂O. Maintenance of IP enrichment post-amplification was controlled by real-time PCR with *Cyp1a1* promoter primers, and the size of the products was verified using the Agilent 2100 bioanalyzer. Amplified DNA (7.5 µg) was fragmented and labeled by GeneChip® WT Double-Stranded DNA Terminal Labeling Kit (Affymetrix) following the manufacturer's specifications. Fragmentation analysis was performed using a RNA 6000 LabChip Kit (Agilent) and an Agilent 2100 bioanalyzer.

Quantitative real-time PCR analysis

Approximately 6% of the 750 top ranked genes scoring by whole genome hybridization were chosen for validation by real-time PCR based on a z-score > 4 and membership in a significantly enriched Gene Ontology (GO) term or KEGG pathway, as indicated in Fig. 3. QRT-

PCRs were performed in triplicate independent biological samples in a reaction mixture containing 1X Power SYBR® Green PCR Master Mix (Applied Biosystems), and 0.1 μ M of each primer (see list of primers in *Supplemental Table S3*). Amplification was performed on an ABI 7500 real-time PCR system (Applied Biosystems) where the reaction was heated to 95°C for 10 min and immediately cycled 35 times through a denaturing step at 95°C for 15 s and an annealing-elongation step at 60°C for 60 s. Melting curve analyses were performed after PCR amplification to ensure that a single product with expected melting curve characteristics was obtained as preliminarily determined during primer tests. For analysis of results, we used the sequence detection software (SDS software version 1.3.1, Applied Biosystems). Relative differences in QRT-PCR among samples were determined using the $\Delta\Delta C_T$ method. The ΔC_T value for each sample was determined using the C_T value (obtained from the means of replicates) from the input DNA to normalized ChIP assay results. The $\Delta\Delta C_T$ was calculated by subtracting control ΔC_T values from the corresponding experimental ΔC_T . The resulting values were converted to fold-changes over control by raising 2 to the power of $-\Delta\Delta C_T$. Analysis was performed using R statistical software and the *limma* Bioconductor package with the eBayes function for variance estimation. *P*-values were adjusted to calculate q-values, as described (Benjamini and Hochberg, 1995), which provides conservative estimates by setting the parameter $\pi_0 = 0$ (Storey and Tibshirani, 2003).

Transcriptome analysis: experimental design and procedure

Comparative transcriptome profiling of DMSO-, BaP- and TCDD-treated Hepa-1c1c7 and c35 cells was performed using the Affymetrix GeneChip Mouse Genome 430 2.0 Array . Eight hours post-treatment, three individual RNA extractions from three biological replicates of 5×10^6 cells were prepared. Total RNA was extracted using NucleoSpin RNA II columns (Macherey-Nagel). RNA extracts were validated for quality and integrity using the Agilent 2100 Bioanalyzer.

Total RNA samples were amplified one round, and the amplified RNA (aRNA) was biotinylated using Ambion Biotin-Enhanced Message Amp II kit (Austin, Texas), following the manufacturer's protocols. Affymetrix GeneChip Mouse Genome Arrays were hybridized with 15 g of fragmented aRNA for 16 hr at 45°C. Hybridization, staining, and washing were carried out using the Affymetrix GeneChip Hybridization Wash and Stain Kit following the manufacturer's protocols.

The data were analyzed to identify differentially expressed genes among experimental conditions. Analysis was performed using R statistical software and the *limma* Bioconductor package (Smyth, 2004). All steps of data preprocessing, including background correction, normalization, and expression set summaries, were performed using RMA. Chip quality was assessed using the *affyQCReport* package of Bioconductor. Estimated fold changes for each comparison were calculated using ANOVA, and significance was assessed using IBMT (Sartor et al., 2006). Genes satisfying an *FDR* < 0.05 level of significance and showing a minimum fold change > 50% were considered differentially expressed.

Binding site identification

Raw data were quantile normalized and all array-pairwise Pearson correlation coefficients were determined to be > 0.95. Initially, a histogram was created to show the chromosomal location of probes with high fold changes in control DMSO treated cells immunoprecipitated with anti-AHR compared to control IgG (ratio>1.5-fold) (see Supplemental Material Figure 5A). This histogram shows that high fold changes were more likely to occur farther from the TSS of a gene (an unintuitive result with likely many false positives), and illustrates the importance of the following analysis steps. The *Limma* package (Smyth, 2004) of Bioconductor was used to perform ANOVA on normalized probes, and significance levels for probes were calculated using an intensity-based Bayesian moderated T-statistic (IBMT) (Sartor et al., 2006). This method obtains precise estimates of variance by pooling information across

genes and accounting for the dependency of variance on probe intensity level (see Supplemental Material Figure 5B). The lowest 20% average intensity probes were removed from subsequent analyses. Significant gene sites were identified using a two-step process. Initially, potential regions bound by AHR were defined as having a median *p*-value < 0.05 over a length of at least 175 bp. In the second step, we used a z-score to assess the cumulative binding evidence across each gene promoter to identify genes with the highest scoring binding profiles. The calculation of the z-score is described below.

Gene scoring algorithm

Probe locations were mapped to the nearest gene using UCSC's Refseq annotation file for NCBI *Mus musculus* genome build v.35 containing a total of 19,979 transcripts, and the region (-6kb, 2.5kb) surrounding the TSS was considered. We calculated overall z-scores for each gene representing the cumulative evidence for AHR binding in a gene promoter region. First, we determined the number of significant regions for each gene promoter (x_g) and the proportion of all regions with median *p*-value < 0.05 (p_c) for each comparison. The z-score measuring the deviation of the observed number of significant regions (x_g) from the number expected by chance ($n_g p_c$, where n_g is the number of regions covered in the promoter of gene g) was calculated as

$$z-score = \frac{x_g - n_g p_c}{\sqrt{n_g p_c (1 - p_c)}}$$

The parameter values for p_c for DMSO vs IgG, BaP vs IgG, TCDD vs IgG, DMSO c35 vs IgG, and TCDD c35 vs IgG respectively, were 0.0416, 0.0283, 0.0249, 0.0037, and 0.0086. Genes were then ranked by descending z-scores, and the top scoring 750 genes from each comparison (wild-type naïve: anti-AHR-IgG, wild-type B[a]P-treated: anti-AHR-IgG, wild-type TCDD-treated: anti-AHR-IgG, c35 mutant naïve: anti-AHR-IgG) were used for functional enrichment analysis.

TRANSFAC motif scoring

For each of the 267 mouse transcription factors with at least one PWM in the TRANSFAC version 12.1 database, we scored genes as to how likely they were to have such a motif within 2 kb of their TSS. Suppose that θ_{jl} is the l^{th} PWM defining the DNA binding motif of length $L(\theta_{jl})$ associated with the j^{th} TF and S_{ijk} is any DNA fragment of length $L(\theta_{jl})$ in the 4 kbp DNA region around the TSS for the i^{th} gene. The score measuring the likelihood of S_{ijk} being the binding site for the j^{th} TF is calculated as

$$R_{ijlx} = \log 2 \left(\frac{p(S_{ijk} | \theta_{jl})}{p(S_{ijk} | \theta_0)} \right) * \frac{1}{\sqrt{L(\theta_{jl})}}$$

where $p(S_{ijk} | \theta_{jl})$ is the probability of S_{ijk} being generated by the product multinomial model with the PWM θ_{jl} and $p(S_{ijk} | \theta_0)$ is the probability of S_{ijk} being generated by the background 3rd order Markov chain with the transition matrix θ_0 estimated using 4 kb fragments around TSS for all genes in the genome. The gene-specific scores for the i^{th} gene and the j^{th} TF are then calculated as:

$$z_{ij} = \log 2 \left(\sum_{l=1}^{m_j} \sum_{k=1}^{n_{ijkl}} \sqrt{\frac{p(S_{ijkl} | \theta_{jl})}{p(S_{ijkl} | \theta_0)}} \right)$$

where the S_{ijkl} is the k^{th} fragment from the promoter of i^{th} gene which for which $R_{ijkl} > 1.5$ and m_j is the number of different PWMs associated with the j^{th} TF.

Functional analysis and clustering

Gene Ontology (GO) terms and KEGG pathways were tested for enrichment of binding and/or differential expression using Fisher's exact test. For ChIP/chip conditions, the list of 750 top ranked genes were used, for the 5-nucleotide motif we identified 562 genes with greater than

or equal to 12 sites within 2kb of the TSS, and for the longer motif, 693 genes with at least 2 sites in the promoter with at least one of those within 2kb of the start site. For expression results, the top 750 ranked up/down regulated in wild type vs. c35 cells were also used. Gene lists identified by analyzing ChIP/chip, expression and promoter sequence data were further clustered based on the level of enrichment of categories in the biological process Gene Ontology (heatmap in Fig. 5). Eighty categories containing more than 10 and less than 1000 genes that were enriched within at least one of the gene lists (FDR<0.2) were first identified. For each gene list, an “enrichment profile” was constructed consisting of –log(Fisher's test p-value of enrichment) for each of these 80 GO categories. Gene lists and GO categories were then clustered based on such “enrichment profiles” using the simple Euclidian distance based average-linkage hierarchical clustering. Columns representing gene lists and rows representing GO categories in Fig. 10 were ordered based on the results of this cluster analysis. To view the clustering interactively please go to the URL <http://eh3.uc.edu/supplements/ahrchip> and then follow the link [Hierarchical clustering of enriched Gene Ontology terms](#) at the bottom of the page.

References

- Bernhard HP, Darlington GJ, Ruddle FH. 1973. Expression of liver phenotypes in cultured mouse hepatoma. Dev Biol 35:83-96.
- Sun W, Zhang J, Hankinson O. 1997. A mutation in the aryl hydrocarbon receptor (AHR) in a cultured mammalian cell line identifies a novel region of AHR that affects DNA binding. J Biol Chem 272:31845-31854.
- Marlowe JL, Knudsen ES, Schwemberger S, Puga A. 2004. The aryl hydrocarbon receptor displaces p300 from E2F-dependent promoters and represses S-phase specific gene expression. J Biol Chem 279:29013-29022.
- Wells J, Farnham PJ. 2002. Characterizing transcription factor binding sites using formaldehyde crosslinking and immunoprecipitation. Methods 26:48-56.
- Schnekenburger M, Talaska G, Puga A. 2007. Chromium cross-links histone deacetylase 1-DNA methyltransferase 1 complexes to chromatin, inhibiting histone-remodeling marks critical for transcriptional activation. Mol Cell Biol 27:7089-7101.

- Benjamini Y, Hochberg Y. 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J Royal Statistical Soc B* 57:289-300.
- Storey JD, Tibshirani R. 2003. Statistical significance for genomewide studies. *Proc Natl Acad Sci U S A* 100:9440-9445.
- Smyth GK. 2004. Linear models and empirical Bayes methods for assessing differential expression in microarray experiments. *Stat Appl Genet Mol Biol* 3:Article3.
- Sartor MA, Tomlinson CR, Wesselkamper SC, Sivaganesan S, Leikauf GD, Medvedovic M. 2006. Intensity-based hierarchical Bayes method improves testing for differentially expressed genes in microarray experiments. *BMC Bioinformatics* 7:538.

Supplemental Material Table 1. Top ranked 750 genes with promoters that bind AHR

Rank	Top ranked genes from naïve DMSO-treated cells					Top ranked genes from [Ba]P-treated cells					Top ranked genes from TCDD-treated cells				
	Entrez ID	Symbol	z-score	BaP rank	TCDD rank	Entrez ID	Symbol	z-score	DMSO rank	TCDD rank	Entrez ID	Symbol	z-score	DMSO rank	BaP rank
1	15511 Hspa1b		12.02	1020	239	18799 Plcd1		13.50	28	6350	11949 Atp5c1		14.09	48	2129
2	381629 0610007C21Rik		12.01	22	60	214384 Myoed		12.89	101	320	245525 B230358A15Rik		13.01	29	9580
3	69786 Tprkb		11.66	245	10944	26403 Map3k11		11.38	266	125	219132 D14Ert668e		10.53	4042	15381
4	194655 Tieg3		11.35	144	850	18119 Nodal		10.82	4532	8955	223669 Zfp7		10.36	9083	3061
5	225872 Npas4		10.38	65	2462	16007 Cyr61		10.77	666	1919	23246 Tmem16e		10.21	6796	2964
6	19377 Rai1		10.28	4559	3658	11637 Ak2		10.58	1477	24	108155 Ogt		10.09	6348	18471
7	102644 D9Ucl1		10.25	189	2150	17347 Mknk2		10.52	446	1561	58186 Rad18		10.00	890	5418
8	66440 Cdc26		9.77	7886	7656	20927 Abcc8		10.27	3735	5472	97423 R74862		9.98	765	118
9	66156 Anapc11		9.60	8704	18	18742 Ptx3		10.23	202	541	269855 A430110N23Rik		9.94	651	10608
10	227525 Dclre1c		9.53	411	258	269642 1110038O08Rik		10.10	214	167	56873 Lmr1		9.86	4193	724
11	11998 Avp		9.52	3980	8467	67184 Ndufa13		9.92	871	1366	103737 Pex12		9.70	3671	8943
12	68879 Prpf6		9.48	689	9080	19679 Ptppm2		9.77	6212	18309	102058 Exoc8		9.61	1073	90
13	233067 Lrfn3		9.41	36	833	214901 Chif18		9.66	553	2896	244713 Zfp75		9.57	2019	15121
14	66706 4733401H18Rik		9.23	2996	688	75530 1700024C24Rik		9.66	108	1062	242691 Gpatc3		9.49	15169	5235
15	16979 Lrrm1		9.16	6539	1052	56188 Fxyd1		9.56	1847	4479	17827 Mtx1		9.40	398	623
16	11781 Ap4m1		9.15	836	1041	242662 Rims3		9.55	1327	191	13209 Ddx6		9.38	960	682
17	72552 Hsd1		8.97	11609	2566	100317 AU040320		9.43	55	9073	381738 Gm1060		9.34	290	4742
18	12959 Cryba4		8.94	999	23	50780 Rgs3		9.39	3692	3856	66156 Anapc11		9.31	9	8704
19	101489 Ric8		8.93	14243	1449	58202 A730008L03Rik		9.11	85	1757	193740 Hspa1a		9.14	110	19581
20	16593 Kns2		8.64	1002	4986	433091 Pnpla1		9.05	219	7235	234023 9430010O03Rik		9.10	393	10284
21	20250 Scd2		8.57	25	3593	399673 Tdpoz2		9.03	13793	12216	68114 Mum1		9.07	65	3970
22	67285 Sdccag10		8.56	12205	12161	381629 0610007C21Rik		9.00	2	60	242653 Cldn19		9.06	94	3382
23	66660 Sltnr		8.53	83	175	17898 Myl7		8.95	3475	629	12959 Cryba4		9.01	18	999
24	78912 Sp2		8.49	755	16247	234384 BC051227		8.91	5413	6775	11637 Ak2		8.90	1477	6
25	107242 Al837181		8.44	1315	936	20250 Scd2		8.85	21	3593	434234 2610020H08Rik		8.85	8970	8303
26	20198 S100a4		8.44	3219	343	13011 Cst7		8.72	2586	15271	72198 Skiv2l2		8.74	13266	11804
27	18208 Ntn1		8.42	482	295	57754 Cend1		8.61	3361	4002	60411 Cenpk		8.62	440	9255
28	18799 Plcd1		8.42	1	6350	78304 Lsmd1		8.59	607	652	14734 Gpc3		8.51	5568	5377
29	245525 B230358A15Rik		8.37	9580	2	259302 Srgap3		8.57	3678	6161	11819 Nr2l2		8.50	44	75
30	207921 A830093124Rik		8.23	2567	11199	239336 Rxfp3		8.45	3074	2832	546134 Gramd2		8.41	3328	4564
31	60527 Fads3		8.14	887	418	19065 Pypy1		8.45	3805	7985	104384 Rhox9		8.41	287	32
32	208691 Elif5a2		8.12	1223	8148	104384 Rhox9		8.45	287	31	232821 Ccdc106		8.40	334	2092
33	67201 2700085E05Rik		8.11	8984	59	14238 Foxf2		8.42	7012	899	234129 Tpte		8.26	3984	870
34	67976 Trabd		8.10	3890	12468	319749 C30078M08Rik		8.38	2054	7940	17242 Mdks		8.25	162	8855
35	381356 5930434B04Rik		8.10	102	5626	231605 Galnt9		8.38	678	8077	50760 Fbxo17		8.20	1460	894
36	12034 Phb2		8.08	341	220	233067 Lrfn3		8.36	13	833	17925 Myo9b		8.18	1260	190
37	71164 Zdhhc11		8.04	1212	8038	68525 Evc2		8.35	319	796	216643 Gabrp		8.18	1504	264
38	243312 A930017N06Rik		8.03	56	202	26362 Axl		8.31	1853	1923	18631 Pexi1a		8.05	8061	12204
39	13875 Erf		8.03	520	133	13483 Dpp6		8.31	73	2662	22390 Wee1		8.04	979	1653
40	223723 Ttl12		7.98	47	3872	105428 AA536717		8.29	1245	8450	68964 1500010J02Rik		8.03	3996	7133
41	15566 Htr7		7.96	67	314	18014 Neurog1		8.27	107	1672	13591 Ebfi1		7.94	456	4403
42	18526 Pcdh10		7.95	4440	42	269019 Stk32a		8.25	2149	495	18526 Gpcd10		7.93	42	4440
43	67011 Mettl6		7.95	1339	1829	81701 Egfl8		8.13	7057	2307	56361 Pus1		7.93	309	2977
44	11819 Nr2f2		7.92	75	29	212569 Zfp273		8.11	7047	4635	380768 Gm1568		7.91	5098	176
45	22289 Tlx		7.92	7317	162	235631 Tsp50		8.09	256	4120	108657 Rnpepl1		7.91	1125	128
46	74253 2310020F24Rik		7.83	1355	6561	67899 2010110K16Rik		8.06	1206	13123	56335 Mettl3		7.89	16234	1148
47	14184 Fgr3		7.81	62	870	223723 Ttl12		8.05	40	3872	67867 Lrrc28		7.83	627	8843
48	11949 Atp5c1		7.81	2129	1	11540 Adora2a		7.93	5516	5180	209416 Gpkow		7.83	3922	10776
49	319170 Hist1h2an		7.81	9211	2232	11746 Anxa4		7.93	14198	16680	258340 Olfr1265		7.81	431	931
50	432677 7420416P09Rik		7.80	1996	11759	70717 6303406I15Rik		7.88	6852	8124	22088 Tsg101		7.77	656	14997
51	70238 Rnf168		7.79	4611	68	99296 Hrh3		7.84	13074	11614	77744 6720463M24Rik		7.75	13910	8900
52	67388 1110085F13Rik		7.77	2763	4178	17877 Myf5		7.81	6957	5088	93708 Pcdhg5		7.75	81	1207
53	109685 Hyal3		7.73	10669	7571	107702 Rnh1		7.80	238	557	12465 Cct5		7.71	11775	13251
54	66606 Lrrc57		7.72	175	2737	84652 Drctnb1a		7.78	244	710	73991 Sppg3a		7.71	720	13269
55	100317 AU040320		7.67	17	9073	66769 4933437N03Rik		7.78	7582	9607	30044 Opn4		7.69	8386	339
56	574402 Gpr17		7.65	659	431	243312 A930017N06Rik		7.72	38	202	381101 BC048355		7.67	1758	8199
57	69815 Krtcap3		7.64	11916	9370	228802 BC104865		7.64	447	668	80794 Cblc		7.66	4826	5123
58	100929 Tyw1		7.64	10132	10149	26556 Homer1		7.63	608	11524	28042 D5Wsu178e		7.65	962	513
59	67917 Zccch3		7.64	1415	2787	80893 Tmprss5		7.62	61	94	67201 2700085E05Rik		7.65	33	8984
60	66146 Tmem57		7.63	1702	7211	331747 Rqag4		7.52	1727	1162	381629 0610007C21Rik		7.61	2	22
61	80893 Tmprss5		7.58	59	94	66783 4933437N03Rik		7.52	1728	1163	21957 Ntn3		7.61	583	254
62	102162 Taf5l		7.56	11926	1644	14184 Fgr3		7.52	47	478	230766 BC030183		7.60	253	4341
63	155707 Ccdc92		7.55	1483	2424	194735 4930430D24Rik		7.51	16474	4544	74326 Hnrnp		7.59	1667	6172
64	13865 Ntn2f1		7.50	8552	1991	67135 2310021H06Rik		7.50	1186	10828	16815 Lbx2		7.58	241	1957
65	68114 Mum1		7.48	3970	21	255872 Npas4		7.46	5	2462	258617 Olfr356		7.58	727	8408
66	80889 Mesdc1		7.47	1132	5264	67826 1110031B06Rik		7.42	13686	12141	73940 Hapl1n2		7.53	4879	1823
67	233016 Blvr		7.47	2320	633	15566 Htr7		7.42	41	314	66403 Asf1a		7.52	4089	7480
68	234796 BC025816		7.46	8599	3603	108072 Grm6		7.42	3920	18086	70238 Rnf168		7.51	51	4611
69	73419 1700052N19Rik		7.45	1252	8118	229228 Nudt6		7.37	172	1854	16599 Klf3		7.49	1011	5090
70	66972 Slc25a23		7.45	234	3779	19041 Ppl		7.37	1159	15814	104416 Bap1		7.47	5459	9830
71	11972 Atp6v0d1		7.45	6145	7804	70445 Cd248		7.27	409	5492	94092 Trim16		7.46	3440	10991
72	211255 Kbtbd7		7.42	378	2412	68040 Zfp593		7.26	4226	172					

94	242653 Cldn19	7.02	3382	22	319475 Zfp672	7.00	11767	6216	80893 Tmprrs5	7.08	61	59
95	269585 Zfp31	7.01	4794	1552	53607 Snrpa	6.99	711	655	104885 Al839735	7.06	177	3768
96	12000 Avpr2	6.98	5267	6007	80880 Ankrd47	6.98	1867	2494	230577 Pars2	7.01	3553	218
97	23872 Ets2	6.97	1593	11503	218865 Chdh	6.96	1197	10881	20810 Srm	6.99	5241	334
98	104445 Cdc42ep1	6.94	5330	1835	20197 S100a3	6.96	9549	3827	19395 Rasgrp2	6.97	3585	12537
99	320664 F730031O20Rik	6.94	3054	242	11689 Alox5	6.94	375	1868	210808 9030625A04Rik	6.97	78	2032
100	26433 Plod3	6.94	200	491	110006 Gusb	6.92	508	3474	54631 Nphs1	6.95	2841	6900
101	214384 Myocd	6.93	2	320	140723 Cacng5	6.90	722	2576	83561 Tdrd1	6.95	4892	15122
102	320974 B430119L13Rik	6.90	548	233	381356 5930434B04Rik	6.90	35	5626	22413 Wnt2	6.94	1020	578
103	381798 4930590J08Rik	6.90	2509	14597	21824 Thbd	6.90	971	4220	59058 Blh1hb5	6.91	2142	11203
104	57247 Zfp276	6.90	5423	18464	242726 Pad16	6.89	378	255	18717 Pip5k1c	6.90	3388	1734
105	76800 Usp42	6.88	2528	6020	67809 1200015F23Rik	6.88	10454	4817	224129 Adcy5	6.88	1832	14804
106	74249 Lrrc2	6.87	1171	3346	237958 4933407P14Rik	6.88	92	433	94185 Tnfrsf21	6.87	1808	8694
107	18014 Neurog1	6.86	41	1672	231991 Creb5	6.85	1923	3857	75541 1700019G17Rik	6.87	4996	89
108	75530 1700024C24Rik	6.86	14	1062	230752 2610027C15Rik	6.85	540	7070	56306 Tera	6.84	5835	9910
109	56032 Tusc4	6.86	3512	1063	117606 Boc	6.85	140	8956	19724 Rfx1	6.82	9039	14657
110	193740 Hspa1a	6.86	9581	19	271047 Serpinab3	6.84	746	7222	67973 Mpshoph10	6.78	1286	11806
111	387285 Hcrtr2	6.85	3514	5064	14657 Gira4	6.84	6607	573	20620 Plk2	6.77	471	2384
112	65967 Eefsef	6.83	12331	1376	76405 1700018B08Rik	6.83	748	6626	74361 4931429L15Rik	6.77	11656	4059
113	56358 Copz2	6.82	4066	278	21334 Tac2	6.82	12007	6864	15002 H2-Ob	6.74	7204	3320
114	68222 BC061039	6.82	8907	6094	19367 Rad9	6.81	10553	7246	67288 3110031B13Rik	6.74	9442	7002
115	78892 Crispid2	6.81	817	3259	56215 Acin1	6.80	1275	4692	259019 Olfr1045	6.73	8940	7908
116	22370 Vtn	6.78	13705	405	30059 Timm10	6.78	213	12619	72128 2610008E11Rik	6.71	5276	1072
117	73658 2210013K02Rik	6.77	14808	9160	170761 Pdz3	6.78	6684	16600	73750 Whrn	6.67	415	373
118	67040 Ddx17	6.77	6244	438	97423 R74862	6.76	765	8	17967 Ncam1	6.67	5518	4278
119	14451 Gas1	6.75	2012	11704	20517 Slc22a1	6.76	3193	4922	244810 AW551984	6.65	6670	4069
120	232946 Bloc1s3	6.74	2613	12410	74408 4933414l15Rik	6.72	130	3206	245527 Eda2r	6.59	2612	9787
121	381979 Brsk1	6.72	4971	4480	17700 Gdf8	6.71	16187	2384	12443 Ccn1	6.59	2613	11517
122	118451 Mrps2	6.71	987	232	121021 Cspg4	6.70	1349	2753	109889 Mzf1	6.58	198	3162
123	171263 V1r1e0	6.70	3119	449	18948 Prmt	6.69	14455	15177	73866 4930432H15Rik	6.58	10329	8322
124	214854 Lincr	6.70	131	612	20017 Rp01-2	6.69	2538	6648	67217 2810055F11Rik	6.53	163	5112
125	320683 Zfp629	6.68	289	5227	382088 Omt2b	6.67	5836	860	26403 Map3k11	6.52	266	3
126	22417 Wnt4	6.68	410	6890	69537 Dnase1l1	6.65	3955	3181	84704 Snurf	6.52	3810	2008
127	72075 Ogt	6.68	1545	747	619324 C130040N14Rik	6.65	3957	12068	22658 Pcg12	6.50	1250	715
128	140743 Rem2	6.68	2681	2720	108657 Rnpepl1	6.65	1125	45	68044 2510006C20Rik	6.50	7621	8846
129	66371 23100101I6Rik	6.64	1557	17131	26386 Hsf4	6.64	1517	10157	74469 Taft1	6.49	7868	16204
130	74408 4933414l15Rik	6.63	120	3206	67674 0610038D11Rik	6.64	587	1855	67181 Dullard	6.46	2050	13698
131	268391 A830031A19Rik	6.61	217	323	214854 Lincr	6.63	124	612	12564 Cdth8	6.46	12199	13716
132	22144 Tuba3	6.61	7470	15428	80906 Kcnip2	6.63	133	11558	18354 Olfr54	6.46	2831	5941
133	80906 Kcnip2	6.60	132	11558	68770 Pht2	6.62	950	6043	13875 Erf	6.46	39	520
134	56541 Habp4	6.59	16044	2015	56325 Abcb9	6.61	5220	3791	385493 AU015836	6.45	6385	16260
135	224481 Tf1b1	6.57	2630	14312	12163 Bmp8a	6.60	4888	5702	11787 Apbb2	6.44	1744	4410
136	18575 Pde1c	6.56	2521	1189	30841 Fbx10	6.57	2113	3019	101513 2700078K21Rik	6.44	9152	6973
137	20933 Surf5	6.56	4248	3669	14772 Gprk2l	6.56	1023	5345	67198 2810022L02Rik	6.41	641	6281
138	27261 Dok3	6.54	279	5824	353155 Egfl7	6.54	8994	3936	66975 2410002C22Rik	6.40	4285	2421
139	192663 Abcg4	6.52	856	4049	15465 Hrh1	6.53	4715	41049	56433 Vps29	6.39	945	12080
140	117606 Boc	6.52	109	8956	26934 Racgap1	6.53	4713	3783	71653 4930506M07Rik	6.39	87	463
141	382252 A830080D01Rik	6.47	14374	14230	74470 4933440J22Rik	6.53	1510	648	17281 Fyco1	6.39	311	2311
142	114774 Pawr	6.47	3309	1354	332713 BC051628	6.52	2291	15871	229600 BC028528	6.37	360	2926
143	226519 Lamc1	6.47	12977	15166	227632 Kont1	6.49	6125	11122	67040 Ddx17	6.37	11464	12917
144	18510 Pax8	6.45	447	630	194655 Tieg3	6.47	4	850	192232 Hps4	6.36	5074	784
145	56873 1110048D14Rik	6.44	9405	4237	68165 B230118G17Rik	6.46	3570	2110	18712 Pim1	6.32	9951	8012
146	11816 Apoe	6.44	1934	5441	56089 Ramp3	6.46	2681	9476	11484 Aspa	6.32	15016	15751
147	228662 Btbd3	6.43	8734	3929	110310 Krt7	6.46	13596	9477	330440 Gm766	6.32	7550	9185
148	16502 Kcncl1	6.42	1031	18724	16820 Lcn3	6.43	4620	3412	68969 Eif1b	6.31	3072	5751
149	54411 Atp6ap1	6.41	202	1224	109284 C030461o1Rik	6.38	1115	12267	74243 2210009G21Rik	6.29	2385	13010
150	67675 Cuta	6.39	3383	4385	13057 Cyba	6.37	254	2234	98828 G431001109Rik	6.29	1962	10950
151	272538 AW413431	6.39	1799	446	80981 Arf4	6.36	3891	2568	15209 Hesx1	6.28	7252	9873
152	22409 Wnt10a	6.38	227	871	67653 4930544G11Rik	6.35	15094	10992	244219 Zfp668	6.27	419	2522
153	14254 Flt1	6.35	1749	884	13142 Dao1	6.35	1358	6990	16391 Isgf3g	6.26	4516	6453
154	71738 Mamdc2	6.33	529	170	320825 E130306M17Rik	6.35	1995	223	234371 Tmem161a	6.24	2786	557
155	64138 Ctsz	6.32	3680	5984	28193 D10ucla1	6.34	4733	4563	15228 Foxg1	6.23	956	1135
156	12224 Klf5	6.31	5255	293	414102 E230016K23Rik	6.34	3387	11713	434784 Ldc1	6.23	8598	12067
157	67678 Lsm3	6.30	12904	1405	22040 Trex1	6.32	10509	6445	27428 Shroom3	6.21	3499	1131
158	18506 Pax4	6.29	5144	11288	99377 Sall4	6.32	3769	6370	27050 Rps3	6.21	1083	16502
159	242785 Klh121	6.26	1114	733	11670 Aldh3a1	6.31	6023	4034	71449 5630401D24Rik	6.21	5217	4607
160	270151 BC034204	6.26	6029	3915	104079 Npxp3	6.31	4148	8345	15415 Hoxb7	6.21	6040	2571
161	27984 Efhd2	6.25	15474	270	16565 Kif21b	6.31	12135	18488	74349 4632419K20Rik	6.20	2106	1325
162	17242 Mdk	6.25	8855	34	217214 Nags	6.31	6107	13808	22289 Utx	6.19	45	7317
163	67217 2810055F11Rik	6.25	5112	124	396184 Flrt1	6.29	1280	3159	20345 Selpl	6.17	10032	10728
164	69091 Vps26b	6.25	9956	2897	74178 Stk40	6.29	296	3613	217353 Tmc6	6.15	5774	6946
165	15401 Hoxa4	6.23	6130	2275	22241 Ulk1	6.28	6881	9056	276950 Sif8	6.15	6431	5340
166	27389 Dusp13	6.22	14156	2182	57773 Wdr4	6.27	5332	7760	101706 Numa1	6.15	191	15286
167	319152 Hist1h3h	6.22	12357	12282	207839 Galnt6	6.27	17443	16171	269642 1110038O08Rik	6.15	214	10
168	83490 Ptk3ap1	6.22	461	1485	18597 Dhah1	6.25	1854	1924	27632 Rdpb	6.15	3705	13185
169	23885 Gmc1	6.22	708	5752	321019 Eb2	6.25	1794	2254	627984 Nalp1c	6.15	3389	10344
170	18141 Nup50	6.20	7164	6448	54637 Praf2	6.25	5750	17385	71738 Mamdc2	6.13	154	529
171	17388 Mmp15	6.18	3470	10724	64296 Abhd8	6.25	4674	7236	71492 Bbs7	6.11	302	421
172	229228 Nudt6	6.18	69	1854	76407 Spag4l	6.23	8105	601	246703 Apoa1bp	6.10	3997	1403
173	239839 G630039H03Rik	6.17	4687	415	148							

190	22772 Zic2	5.98	2941	455	17925 Myo9b	6.04	1260	36	74388 Dpp8	5.95	704	10982
191	101706 Numa1	5.98	15286	166	71592 Pogk	6.03	11001	3873	242662 Rims3	5.94	1327	16
192	68846 1110061N23Rik	5.98	2014	15080	56292 Ard1	6.03	1161	17040	70511 5730409G15Rik	5.94	13952	4406
193	330503 B430201F14	5.97	12004	477	57330 Perq1	6.01	7357	7535	54325 Elovl1	5.93	4488	468
194	15166 Hcn2	5.96	1764	7550	67511 Timed9	6.01	3424	1892	14874 Gstz1	5.93	1209	6529
195	234695 D130029J02Rik	5.94	404	14200	23928 Lamc3	5.98	1202	4995	99982 Aof2	5.93	5831	14827
196	20537 Slc5a1	5.93	5555	14828	73247 1600027N09Rik	5.98	11925	11508	66790 Grtp1	5.91	9200	5631
197	14708 Gng7	5.93	958	6537	57814 Kcne4	5.98	3982	6553	414801 BC063749	5.90	8280	14731
198	109889 Mzf1	5.93	3162	122	20016 Rpo1-1	5.98	539	3749	332578 Lcn10	5.90	3522	2208
199	240756 Klh12	5.93	8812	841	81000 Rad54l2	5.96	4965	5546	235461 B230380D07Rik	5.88	4543	14872
200	238271 Kcnh5	5.91	241	2191	26433 Plod3	5.96	100	491	223809 Smgc	5.88	14920	13528
201	56213 Htra1	5.90	5604	9720	317758 Gimpar9	5.96	5905	4209	76108 Rap2a	5.88	2963	18460
202	18742 Pitx3	5.88	9	541	54411 Atp6ap1	5.96	149	1224	243312 A930017N06Rik	5.87	38	56
203	268890 Lsamp	5.88	1623	6611	19012 Ppap2a	5.96	5467	1701	241052 C230300N03Rik	5.87	9862	7918
204	18303 Nflc3	5.88	7988	10669	66622 573041019Rik	5.95	15704	213	16706 Ksr1	5.84	547	1331
205	319169 Hist1h2ak	5.88	12079	3113	59090 Midn	5.95	3813	14119	19763 Ring1	5.83	673	5698
206	16324 Inhbb	5.86	1493	3097	56273 Pex14	5.95	5049	5258	72881 Zdhc4	5.83	4137	4989
207	212539 Gm266	5.85	425	178	320100 Tnfrsf19l	5.95	183	4571	78777 241002101Rik	5.82	523	7858
208	16651 Sspn	5.85	920	16633	69274 Ctdspl	5.93	4708	3468	15260 Hira	5.81	6244	12595
209	72125 2600011E07Rik	5.85	5820	7700	230779 Serinc2	5.92	306	3456	12064 Bdrlf	5.81	15369	5101
210	232853 5730403M16Rik	5.84	4894	13216	67909 Galnt5	5.91	16269	4275	210933 Ba3	5.81	2425	8013
211	57317 Slrs4	5.84	1758	2695	66128 Mrps36	5.90	443	9042	68304 Kdelc2	5.81	2426	11893
212	58521 Cri1	5.83	1172	2049	13611 Edg6	5.89	954	5366	14263 Fmo5	5.81	1373	2548
213	30059 Timm10	5.80	116	12619	74486 Osbp10	5.88	11325	7575	66622 573041019Rik	5.80	15704	204
214	269642 1110038O08Rik	5.79	10	167	80903 Fgf16	5.88	1759	653	56223 Fscn3	5.80	12930	14283
215	210035 BC030440	5.79	7850	2758	93843 Pnck	5.88	9528	9784	258338 Olfr1259	5.79	11833	7904
216	16572 Kif5a	5.79	10376	10345	246154 Vasn	5.88	7562	18678	23071 Snx26	5.77	5888	17689
217	54402 Stk19	5.78	5779	524	268391 A830031A19Rik	5.86	131	323	23829 C1ql1	5.77	2473	2621
218	66691 Gapvd1	5.77	10381	4986	230577 Pars2	5.85	3553	96	12552 Cdh11	5.77	721	5295
219	433091 Pnpl1	5.77	20	7235	13615 Edn2	5.85	357	1554	381845 2310014L17Rik	5.75	4261	16380
220	107373 4632417K18Rik	5.77	11046	6456	17199 Mc1r	5.83	6070	8390	12034 Phb2	5.75	36	341
221	68352 0610012D14Rik	5.77	909	2833	15985 Cd79b	5.83	6507	5206	12064 Bdrlf	5.75	3875	2047
222	30954 Siva	5.73	916	2105	58250 Chst11	5.82	1026	5874	71986 Ddx28	5.74	3221	588
223	19201 PstPIP2	5.73	693	1615	11636 Ak1	5.82	5816	9093	320825 E130306M17Rik	5.73	1995	154
224	72171 Shq1	5.73	4377	1323	50493 Txnrd1	5.80	2375	900	50772 Mapk6	5.71	6650	5133
225	320169 D330022A01Rik	5.73	967	4894	83554 Fstl3	5.80	3110	8327	68080 Atpb1c	5.71	3580	3417
226	66147 Necap2	5.73	15016	1328	140858 Wdr5	5.80	563	4399	55985 Cxcl13	5.71	4014	3176
227	68106 Nt5c3l	5.72	2872	12700	22409 Wnt10a	5.80	152	871	21937 Tnfrsf1a	5.70	1523	1276
228	72565 Uaca	5.71	2506	674	170752 Rac3	5.79	4419	9714	56615 Mgst1	5.70	8213	8952
229	81909 Zfp1	5.70	1447	13377	16439 Itp2	5.79	996	4159	56373 Cpb2	5.70	5166	17129
230	11652 Akt2	5.70	2503	6362	66142 Cox7b	5.78	3189	1956	12982 Csf2ra	5.69	2051	2361
231	140559 Igf8	5.70	2221	5875	232174 Cyp26b1	5.77	8199	18551	14105 Fusip1	5.67	2625	2672
232	107767 Scamp1	5.70	6337	3262	16005 Igfals	5.73	403	8423	118451 Mrps2	5.63	122	987
233	234366 Gatad2a	5.69	3969	759	237625 Pla2g3	5.73	2993	11868	320974 B430119L13Rik	5.62	102	548
234	107607 Card4	5.69	1879	72	66972 Slc25a23	5.73	70	3779	15561 Htr3a	5.60	8376	1152
235	19703 Renbp	5.68	2216	9043	320844 Amigo3	5.72	2559	5830	234404 Txnl6	5.59	343	4389
236	18971 Pold1	5.68	4224	15379	20499 Slc12a7	5.72	5260	4231	51886 Fubp1	5.59	909	9278
237	21393 Tcap	5.67	370	3828	67272 Cmt5	5.72	330	14947	234736 Rfwd3	5.59	3004	3147
238	107702 Rnh1	5.66	53	557	16668 Krt18	5.72	9819	11107	67686 1700011J10Rik	5.58	2083	9457
239	71932 Abhd9	5.66	7997	5506	107448 Unc5a	5.70	7939	2801	15511 Hspa1b	5.57	1	1020
240	117160 Ttyh2	5.65	354	4985	270004 Foxi2	5.70	3028	9864	13854 Eprn1	5.57	1448	13841
241	16815 Lbx2	5.64	1957	64	238271 Kcnh5	5.69	200	2191	100163 Pafah2	5.57	4492	571
242	19262 Ptpra	5.63	11728	11099	236794 Slc9a6	5.69	2343	728	320664 F730031O20Rik	5.57	99	3054
243	13849 Eph1	5.61	17095	1984	58805 Mlxip	5.69	363	813	59289 Ccbp2	5.56	542	1451
244	84652 Drcnnnb1a	5.61	54	710	226414 Dars	5.69	2460	4011	12617 Cenpc1	5.55	758	1329
245	16001 Igf1r	5.60	18262	1637	69786 Tprkb	5.67	3	10944	218973 Wdh1	5.54	528	11998
246	57373 D930014E17Rik	5.59	15682	15490	72323 Asb6	5.66	6351	7007	11438 Chrn4	5.54	889	2142
247	244723 Olfrm2	5.57	10307	443	28185 Tomm70a	5.66	1436	14390	26913 Gprin1	5.53	2860	1670
248	18386 Oprd1	5.57	1378	9743	98710 Rabif	5.64	5863	7140	11443 Chrn1b	5.53	453	2294
249	66398 Commd5	5.57	667	275	69596 2310035K24Rik	5.63	11792	10544	76816 Sdcag8	5.53	13892	8326
250	18081 Ninj1	5.57	1753	6584	54615 Nppf	5.63	7602	8700	258046 Olfr951	5.51	4231	773
251	11735 Ank3	5.57	3568	403	381866 Mrgpr6	5.63	11643	2637	29807 Tpk1	5.51	1501	1048
252	100608 Noc4l	5.57	10010	4586	668110 4930481F22Rik	5.63	324	977	213499 Fbxo42	5.50	2161	5339
253	230766 BC030183	5.54	4341	62	24131 Lbd3	5.63	15168	17214	77655 BC005537	5.50	6362	15335
254	13057 Cyba	5.54	150	2234	21957 Tnnt3	5.63	583	61	194738 Rhox11	5.50	2169	6931
255	72082 Cyp2c55	5.54	1472	2813	12830 Col4a5	5.62	2222	14407	242726 Pad16	5.47	378	104
256	235631 Tsp50	5.53	45	4120	67477 1300007F04Rik	5.62	7080	1698	78521 B230219H22Rik	5.47	422	432
257	259070 Olfr829	5.53	1944	7512	66983 Ccd16	5.62	416	1535	69301 1700008P20Rik	5.47	9244	1841
258	227631 Sohlh1	5.52	602	384	75769 4833424O15Rik	5.61	1908	5589	227525 Dclre1c	5.46	10	411
259	17826 Mtvr2	5.52	10901	1605	93841 Uchl4	5.60	3703	1246	77683 Ehmt1	5.46	10519	12084
260	110385 Pde4c	5.52	1280	862	21823 Th	5.60	16579	10086	16514 Kcnj11	5.46	6208	808
261	76737 Crel2d	5.50	5238	9760	75171 4930543L23Rik	5.60	4593	3239	56282 Mrp12	5.46	1054	7710
262	72106 2610033J06Rik	5.49	16744	6243	50523 Lats2	5.60	10131	7448	110962 Mbd6	5.44	11166	14650
263	75106 4930519F16Rik	5.49	13079	2101	66673 Sorcs3	5.59	744	3858	109731 Maob	5.43	432	4733
264	208982 Hmgdl1	5.48	9197	4041	216643 Gabrp	5.58	1504	37	65964 B230120H23Rik	5.43	2929	1107
265	229714 Gpr61	5.48	615	2754	234836 Il17c	5.58	918	776	214812 Zfp609	5.43	11599	7743
266	26403 Map3k11	5.47	3	125	71733 Susd2	5.58	770	5543	381280 6430706D22Rik	5.43	7445	9401
267	20418 Shc3	5.47	2393	11163	332942 Gm853	5.57	2039	16353	67946 Spata6	5.43	2989	1257
268	103135 Usp52	5.47	8655	5853	259148 Olfr329	5.56	1982	3335	66966 Trit1	5.43	2257	7024
269	55982 Paxip1	5.46	1098	360	228942 Cbln4	5.55	3951	6504	12661 Chl1	5.41	5440	10491
270</												

286	16785 Rpsa	5.36	2147	765	56812 Dnajb10	5.50	373	4689	217718 Nek9	5.35	9863	17592
287	104384 Rhox9	5.36	32	31	17314 Mgmt	5.50	3656	1693	239273 Abcc4	5.34	7337	14750
288	276952 Rasl10b	5.36	1966	5056	225341 Lims2	5.49	354	1034	15077 Hisi2h3c1	5.34	1639	7692
289	16539 Kcn2s	5.36	5981	5059	320683 Zfp629	5.49	125	5227	228368 Slc35c1	5.33	619	4119
290	381738 Gm1060	5.35	4742	17	15163 Hcls1	5.49	10043	11388	19214 Ptgrdr	5.33	9365	8780
291	58235 Pvr1	5.35	355	4938	622404 LOC622404	5.48	7591	3944	16348 Invs	5.33	2529	1240
292	78906 9130017N09Rik	5.34	14311	13488	12959 Cryba4	5.47	1665	8090	21754 Tesk1	5.32	381	1825
293	216169 D10Bwg1364e	5.33	4065	1006	231603 A630023P12Rik	5.47	3944	8972	12224 Klif5	5.32	156	5255
294	16840 Lect1	5.33	3230	1350	98363 Efhd1	5.46	17639	8099	21887 Tle3	5.31	8636	10403
295	53978 Edg4	5.32	7730	537	216963 Git1	5.46	5475	11423	18208 Ntn1	5.30	27	482
296	74178 Stk40	5.30	164	3613	11418 Accn1	5.46	2055	11424	77411 Rbm35b	5.30	365	1646
297	69961 2810432D09Rik	5.30	9451	522	18019 Nfatc2	5.44	830	4808	18718 Pip5k2a	5.30	3823	1180
298	11698 Ambn	5.29	15495	457	319259 9930021D14Rik	5.44	7652	15823	18968 Pola1	5.29	2404	15543
299	232599 B930018B01	5.29	7272	599	228775 Trib3	5.43	8962	11069	13480 Dpm1	5.29	1059	9900
300	68202 Ndulf45	5.28	6255	8753	211286 Cin5	5.42	2948	4701	243944 4930433I11Rik	5.29	6262	14098
301	63828 Fn3k	5.28	9050	12493	75646 Ra14	5.42	469	4625	70530 Lrrf2	5.28	1583	384
302	71492 Bbs7	5.28	421	171	50765 Trf2	5.41	4296	4645	56524 Mp6p	5.28	5389	4884
303	20563 Slit2	5.27	4046	3189	13866 Erbb2	5.41	3508	372	353320 Defb37	5.28	6386	2760
304	330790 Hapl4n	5.26	17010	453	17537 Mrg2	5.41	7268	11714	76055 Mgaa5	5.28	4077	2769
305	109077 Int5	5.25	2616	13809	14359 Fx1h	5.40	894	1381	77981 B230110C06Rik	5.28	9590	2771
306	230779 Serinc2	5.25	209	3456	53901 Dscr11	5.39	8139	4018	75458 Cklf	5.26	562	889
307	107305 Vps37c	5.25	6795	3460	13078 Cyp1b1	5.39	1693	854	72350 281002I04Rik	5.25	442	12034
308	54397 Ppt2	5.25	6143	1622	104111 Adcy3	5.38	1002	4060	654820 G530011O06Rik	5.25	10411	15596
309	56361 Pus1	5.24	2977	43	20354 Sema4d	5.38	4185	669	56078 Car5b	5.25	585	1682
310	103236 Csnk1g2	5.24	4178	4342	83703 Dbr1	5.38	11433	14651	27225 Ddx24	5.25	2485	1683
311	17281 Fyco1	5.23	2311	141	93835 Amn	5.36	10289	4173	140579 Elmo2	5.25	2540	2109
312	622408 LOC622408	5.22	13436	9426	15441 Hp1bp3	5.36	967	1102	20203 S100b	5.25	1204	2697
313	24083 Gtf3b	5.22	1088	3489	268396 Sh3pxd2b	5.36	4534	10993	59288 Dctn5	5.25	4659	6586
314	269952 D330012F22Rik	5.21	2910	4400	142681 Slc34a3	5.36	428	8983	15566 Htr7	5.24	41	67
315	66156 Anapc11	5.21	11478	7468	16189 I4	5.35	3494	6796	75612 Gns	5.24	4138	701
316	67286 Rab15	5.21	6350	1266	67722 4921517D21Rik	5.34	1088	5302	67210 Gatad1	5.24	5242	3774
317	102448 Xylb	5.19	1876	2010	68339 0610010D24Rik	5.33	2974	9005	19045 Ppp1ca	5.23	1175	180
318	15452 Hprt1	5.19	16047	7430	17216 Mcm2	5.33	2543	14694	67966 Zcchc10	5.23	15581	14176
319	68525 Evc2	5.19	37	796	10963 Upk1a	5.33	16241	14695	437469 RhoX10	5.23	271	5191
320	66656 Eef1d	5.19	1145	1303	626578 Lpc126578	5.32	11858	10596	214384 Myocd	5.22	101	2
321	20745 Spock1	5.18	5294	10629	213484 Nutd18	5.31	4175	5983	68270 Lrrc50	5.22	13785	3875
322	64059 Oxc12a	5.17	338	685	20296 Ccl2	5.31	1380	4773	26381 Esrrg	5.21	8839	7388
323	68592 Syf2	5.16	9042	6222	320693 4732415M23Rik	5.31	490	2135	268391 A830031A19Rik	5.21	131	217
324	668110 4930481F22Rik	5.15	252	977	13627 Eef1a1	5.30	1768	1625	60594 Capn12	5.21	2505	1494
325	20409 Ostf1	5.15	4962	13304	224912 Ctb3	5.30	826	13373	320024 Aadac1	5.21	1353	10478
326	18190 Nrnx2	5.14	1083	1710	11941 Atp2b2	5.29	1121	2002	71728 Stk11ip	5.20	1232	6594
327	11470 Act17a	5.13	5627	13920	11731 Ang2	5.29	2415	4176	26877 B3gal1t	5.20	3940	11513
328	20970 Sdc3	5.11	2334	4298	230737 Gnl2	5.29	7971	5683	24064 Spry2	5.20	16925	11524
329	12695 Inadl	5.11	9100	3128	14680 Gnal	5.29	8883	16720	546049 C330021F23Rik	5.19	11376	10315
330	67272 Cmtm5	5.11	237	14947	330305 A630038D02	5.28	5986	336	21673 Dntt	5.19	4842	2272
331	14571 Gpd2	5.11	7509	753	104394 E24	5.27	1281	83	170720 Card14	5.17	4262	3841
332	442829 Ccin	5.10	7522	1736	66264 Ccdc28b	5.27	1840	6770	76263 Gstk1	5.17	3429	12124
333	13190 Dct	5.09	1629	3469	235379 Gldn	5.26	75	1059	66775 Ptplad2	5.16	3301	528
334	232821 Cdcd106	5.09	2092	32	20810 Srm	5.25	5241	97	16326 Ihnb	5.16	550	4790
335	215723 BC024997	5.09	12670	1040	105501 Abhd4	5.25	1329	2127	70747 Tspan2	5.16	612	5845
336	69454 Clic3	5.09	15470	7872	19819 Rnaseh1	5.25	3270	4221	330305 A630038D02	5.16	5986	330
337	56695 Pnkd	5.09	5051	6682	67077 1700019N12Rik	5.25	10570	13492	13830 Stom	5.16	2597	1736
338	66397 Sar1b	5.09	8488	2649	64059 Oxtc2a	5.24	322	685	12014 Bach2	5.15	9336	11596
339	18442 P2ry2	5.08	5933	3838	30044 Opn4	5.24	8386	55	226265 6430537H07Rik	5.15	792	16687
340	80291 BC003324	5.08	14150	13978	13036 Ctsh	5.24	7483	4515	66208 Nernf	5.14	2775	831
341	228361 D030051N19Rik	5.06	3222	1151	12034 Phb2	5.24	36	220	245886 Ankrd27	5.14	5373	13442
342	13048 Cutl2	5.06	1920	530	269397 Ss181	5.24	868	4516	94352 Lox2	5.13	974	3216
343	234404 Txnl6	5.06	4389	235	210992 Ayt1	5.23	790	588	20198 S100a4	5.13	26	3219
344	72308 Brf1	5.05	4058	2376	97541 Qars	5.23	791	5573	330050 Al847670	5.11	3378	1420
345	73420 1700054N08Rik	5.05	971	5703	67945 Rpl41	5.23	1895	2983	20747 Spop	5.11	8410	10920
346	654812 Angpt17	5.04	771	2326	20528 Slc24a	5.23	1842	416	257932 Olfr332	5.10	11676	8502
347	12578 Cdkn2a	5.04	6204	6802	22064 Trpc2	5.23	4402	3581	56468 Soc5	5.10	9422	11704
348	69601 Dab2ip	5.04	9274	8323	331026 Gmppb	5.22	682	15732	21853 Timeless	5.10	646	17213
349	258500 Olfr944	5.04	14698	2691	11820 App	5.22	559	4923	94246 Arid4b	5.08	9533	9834
350	20931 Surf2	5.02	2321	13451	104001 Rtn1	5.19	3002	1285	18741 Pit2	5.08	11990	13507
351	544763 F83011E18Rik	5.02	1905	874	76308 Rab1b	5.19	5231	509	319149 Hist1h3d	5.08	7316	13518
352	230119 Zbtb5	5.02	7623	5155	231148 Ablim2	5.19	9810	9413	21944 Tfnpf12	5.08	272	1560
353	74666 4930432K21Rik	5.02	11109	1955	207893 Tmem132e	5.19	5232	1737	12462 Cct3	5.08	735	4033
354	225341 Lims2	5.01	288	1034	117160 Ttyh2	5.18	240	4985	12857 Cox4i1	5.08	13911	8901
355	140806 Il25	5.01	17304	17123	58235 Pvr1	5.18	291	4938	243864 Mill2	5.08	1896	12432
356	18509 Pax7	5.01	12267	6366	67692 1700020N01Rik	5.17	10012	9239	19891 Rp2a	5.07	959	1219
357	13615 Edn2	5.01	219	1554	209039 Tenc1	5.17	771	6918	67851 1700021F05Rik	5.07	1926	1808
358	13508 Dscam	5.00	2164	3743	78914 Nadsyn1	5.17	8737	5896	71703 Armcx3	5.07	6797	5204
359	223696 Tomm22	5.00	10629	6317	20200 Polr2a	5.17	2889	1556	26914 H2afy	5.07	2699	16509
360	229600 BC028528	4.99	2926	142	77905 Fte1	5.16	3694	6247	55982 Paxip1	5.07	269	1098
361	19281 Ptpr	4.98	7330	2351	108077 Skiv2l	5.15	1407	1643	140709 Emid2	5.07	1545	5968
362	171209 Accn3	4.98	3192	4001	12181 Bop1	5.15	1410	11878	54215 Cd160	5.05	4572	380
363	58805 Mlxpl	4.98	243	813	69399 1700025G04Rik	5.15	10994	12092	64452 Slc5a4a	5.05	8910	5902
364	23943 Mbc2	4.98	7660	11858	28169 Agpat3	5.15	12536	18057	26900 Ddx3y	5.05	3582	9875
365	77411 Rbm35b	4.96	1646	296	68938 Aspscrl	5.14	4827	1360	12914 Crebbp	5.05	2121	419
366	432769 Zfp708	4.96	10612	1								

382	54122 Uevld	4.91	9031	8335	66462 281042815Rik	5.10	14072	11109	12448 Ccne2	4.98	5195	14388
383	80987 Nckipsd	4.90	5879	1142	73094 Sqip1	5.09	3948	2952	225617 9430028L06Rik	4.98	17047	15905
384	68955 1500001A10Rik	4.90	1260	5014	70530 Lrfn2	5.09	1583	301	227631 Sohlh1	4.98	258	602
385	214345 Lrrc1	4.90	3726	8130	14114 Fbln1	5.09	5571	2629	20288 Msr1	4.97	930	2843
386	70129 Slc44a4	4.90	3727	18091	20840 Stac	5.08	10193	7488	99512 Wdr47	4.97	8080	7676
387	22275 Urod	4.90	5239	13582	269717 Tmem142b	5.07	2002	2261	78252 4432416J03Rik	4.97	3586	6937
388	26926 Pdd8	4.88	646	79	19671 Rce1	5.07	1194	5090	67268 2900073G15Rik	4.97	6974	5365
389	327860 RP23-280J3.2	4.88	7191	4756	26423 Nr5a1	5.06	760	5724	11544 Adprh	4.97	5691	8712
390	11933 Atp1b3	4.87	11635	8966	107173 Gpr137	5.06	965	1957	12448 Ccne2	4.96	5611	2316
391	67732 4833421E05Rik	4.87	1154	8701	72865 Cxx1c	5.04	4012	460	66308 2810021B07Rik	4.96	15049	13641
392	11911 Atf4	4.86	882	2175	17064 Cd93	5.04	2640	18151	52123 Agpat5	4.95	4359	7754
393	234023 9430010O03Rik	4.85	10284	20	72920 Spock3	5.04	5662	16061	68682 Slc44a2	4.94	571	3422
394	226016 5730446C15Rik	4.85	1202	4013	320800 9230112E08Rik	5.04	1324	426	69329 1700003M02Rik	4.94	9114	12562
395	74153 Ube1l	4.84	704	1175	21948 Tfnsf7	5.03	3560	2294	22404 Wiz	4.94	18436	10458
396	23969 Pacsin1	4.84	1198	1607	14731 Gpaa1	5.03	2058	5292	433208 LOC433208	4.94	79	12600
397	72026 Trmu	4.84	649	18404	52830 Pnrc2	5.02	8817	17697	19192 Psme3	4.93	3710	4137
398	17827 Mtx1	4.84	623	15	13116 Cyp46a1	5.02	1160	1017	269997 6430604K15Rik	4.93	8765	8228
399	30840 Fbxl6	4.84	5303	1157	20609 Sstr5	5.02	2160	14356	69363 Spaca4	4.93	854	7777
400	50873 Park2	4.84	3694	3079	332396 Kcnk18	5.01	518	1438	50754 Fbxw7	4.92	5186	11005
401	14603 Gif	4.84	15443	4815	258578 Olfr1026	5.01	7077	8265	15978 Ifng	4.91	2959	851
402	27410 Abca3	4.84	6660	3209	66594 Uscr	5.01	3335	642	52829 D4bwg0951e	4.91	1347	5629
403	16005 Igfls	4.83	232	8423	22253 Unc5c	5.01	2648	8995	11735 Ank3	4.91	251	3568
404	270035 D030041N04Rik	4.82	17956	2623	234695 D130029J02Rik	5.00	195	14200	207615 Wdr37	4.91	7564	3573
405	17150 Mfap2	4.81	5992	1653	14527 Ggr	5.00	502	9739	22370 Vtn	4.91	116	13705
406	56642 Ankrd2	4.81	369	428	18947 Pnlipp2	5.00	5999	7254	11792 Apex1	4.91	15106	13718
407	19771 Rlpb1	4.81	1814	408	27973 Vkorc1	5.00	4756	1903	100169 Phactr4	4.91	1126	422
408	232236 C130022K22Rik	4.81	7890	15748	56226 Espn	4.99	7456	952	19771 Rlpb1	4.91	407	1814
409	70445 Cd248	4.81	71	5492	67287 Parp6	4.99	4342	3905	74140 Tmfsf1	4.90	8104	9202
410	70533 Btf314	4.80	14381	5385	22417 Wnt4	4.99	126	6890	66988 Lap3	4.90	1503	15233
411	15902 Id2	4.80	18729	17039	227525 Dclre1c	4.99	10	258	13872 Erc3	4.89	3712	10552
412	64540 Tspan4	4.80	9183	2712	68010 Bambi	4.98	10732	5843	14961 H2-Ab1	4.88	3725	17158
413	14115 Fbln2	4.79	4706	9382	12841 Col9a3	4.98	4092	12390	319210 4930518C23Rik	4.87	8873	4158
414	66993 Smarcd3	4.79	18316	2239	13592 Ebfl2	4.97	7741	8073	30877 Gnl3	4.87	4581	12687
415	73750 Whrn	4.78	373	117	105782 Scrib	4.97	3962	9771	239839 G630039H03Rik	4.87	173	4687
416	66983 Ccdc16	4.78	257	1535	56861 Olfr480	4.97	1536	2183	20528 Sicc2a4	4.86	1842	346
417	27409 Abcg5	4.78	4668	2530	207565 Camkk2	4.97	1103	7927	66445 Cyc1	4.85	8281	6299
418	68112 Sdcagc3	4.78	4669	9231	29869 Ulk2	4.97	10172	16462	60527 Fads3	4.85	31	887
419	244219 Zfp668	4.78	2522	152	12914 Crebbp	4.97	2121	365	23948 Mmp17	4.85	6426	3346
420	78926 Gas211	4.78	7487	13716	18195 Nsf	4.96	5435	17128	102093 Phikb	4.85	1403	5240
421	14479 Usp15	4.77	11788	5538	71492 Bbs7	4.96	302	171	74022 3930401K13Rik	4.85	7661	13774
422	78521 B230219D22Rik	4.77	432	256	100169 Phactr4	4.96	1126	407	236539 Phgdh	4.85	9826	8993
423	258335 Olfr374	4.77	431	589	446210 AY702103	4.96	18579	1733	74246 Gale	4.84	3820	1521
424	259081 Olfr643	4.76	17093	3737	102103 Mtus1	4.96	5007	1734	77836 Milana	4.84	6984	2204
425	208518 Cep78	4.76	1619	369	212539 Gm266	4.96	207	178	13560 E4f1	4.84	4086	3183
426	20753 Sprn1a	4.76	2636	6083	259303 Srgap3	4.94	5843	9134	320800 9230112E08Rik	4.83	1324	394
427	74002 Psd2	4.76	1793	3072	71853 Pdia6	4.93	5751	826	19934 Rp122	4.83	2247	2594
428	142681 Slc34a3	4.75	314	8983	17075 Tacstd1	4.93	372	4712	56642 Ankrd2	4.83	406	369
429	22418 Wnt5a	4.74	14717	4970	260298 Fev	4.93	16679	8849	16588 Kin	4.82	766	11809
430	107528 Magee1	4.74	10322	9474	12971 Crym	4.92	2275	1083	232685 AB041803	4.82	7527	3983
431	258340 Olfr1265	4.73	931	49	258335 Olfr374	4.92	423	589	574402 Gpr17	4.81	56	659
432	109731 Maob	4.73	4733	263	78521 B230219D22Rik	4.92	422	256	50909 C1r	4.81	8068	3646
433	105670 Rcbt2	4.73	2133	4526	67067 201010012Rik	4.91	4461	2289	237958 4933407P14Rik	4.80	92	106
434	66664 Tmem41a	4.73	9283	6693	20112 Rps6ka2	4.91	4131	13623	14789 Leprel2	4.80	7297	7106
435	20135 Rrm2	4.73	11246	6694	15018 H2-Q7	4.91	1592	4012	14381 G6pdpx	4.80	1449	1021
436	52245 Commd2	4.73	7405	8586	329514 9430083I22	4.91	1691	7740	240690 St18	4.80	3881	11834
437	71897 2310010M24Rik	4.73	15999	662	11936 Fxyd2	4.90	463	1771	98985 Al462438	4.79	13316	4553
438	242521 Klh9	4.73	6132	1258	214952 Rhot2	4.90	2228	1978	67040 Ddx17	4.79	118	6244
439	12796 Camp	4.72	1637	10184	76498 Paqr4	4.90	13975	10309	328370 Rt1	4.77	6026	7171
440	60411 Cenpk	4.72	9255	27	66330 1700020L24Rik	4.88	13025	2864	30928 Arl4c	4.77	10146	3249
441	109079 Sephs1	4.71	1279	1201	108946 Zzz3	4.88	11513	6850	53375 Mtx2	4.77	3125	480
442	72350 2810020I04Rik	4.71	12034	307	14276 Folr2	4.88	3252	8028	170828 Vgll1	4.77	807	9913
443	66128 Mrps36	4.71	211	9042	381405 Gm1008	4.87	6771	10994	244723 Olfrm2	4.76	247	10307
444	242939 Cpz	4.70	1248	3515	20716 Serpina3n	4.87	2938	4048	11676 Aldoc	4.76	1584	4327
445	213649 Arhgef19	4.70	5633	536	268294 Zbtb24	4.87	8190	17248	20677 Sox4	4.75	2111	2591
446	17347 Mknk2	4.70	7	1561	235402 Lrrm6a	4.86	5042	4793	272538 AW4143431	4.74	151	1799
447	228802 BC018465	4.70	57	668	18510 Pax8	4.86	144	630	93675 Clec2i	4.74	1181	997
448	105785 Kdrl3	4.70	3938	929	227707 BC005624	4.85	6441	9715	233752 Insc	4.74	2406	3354
449	24055 Sh3bp2	4.70	3940	6748	12288 Cacna1c	4.85	2910	76	171263 V1re10	4.74	123	3119
450	64652 Nisch	4.70	10881	14323	328440 Npm2	4.85	3154	665	225280 D303070L09Rik	4.73	6903	7312
451	53972 Ngfef	4.70	4600	995	77090 Ocel1	4.84	8128	3299	259033 Olfr1122	4.73	7869	16205
452	22385 Baz1b	4.69	6266	5548	13034 Ctse	4.84	4676	13859	14714 Gnrh1	4.71	4788	14234
453	11443 Chrb1	4.69	2294	248	103161 Apof	4.83	9210	1136	330790 Hapl4	4.71	304	17010
454	14803 Grid1	4.69	10404	9548	54200 Sult2b1	4.83	1666	14571	14420 Galc	4.71	4984	17013
455	212531 Sh3bgr2	4.69	18688	18658	12654 Chi31	4.83	13149	3258	22772 Zic2	4.70	190	2941
456	13591 Ebfl1	4.68	4403	41	20497 Slc12a3	4.81	11970	14556	14300 Frg1	4.70	527	3327
457	240025 Dact2	4.68	6706	3542	237887 Slfn10	4.81	3204	3407	11698 Ambn	4.70	298	15495
458	12209 Brs3	4.68	11572	10792	56434 Tspan3	4.80	2345	4265	68338 Golt1a	4.69	9591	16241
459	66202 111005G10Rik	4.67	8986	5676	22349 Vil1	4.80	8830	8279	381818 MGCT7233	4.68	10703	17056
460	68251 5430437P03Rik	4.67	951	12407	67283 Slc25a19	4.80	3893	3532	72865 Cxx1c	4.68	4012	391
461	72219 1700013B16Rik	4.67	3554	4831	83490 Plik3ap1	4.80	168	1485	12642 Ch25h	4.6		

478	27412 Peg12	4.62	7507	15474	18389 Oprl1	4.72	16946	11226	15450 Lipc	4.59	3349	16367
479	19211 Pten	4.62	6806	855	23993 Klk7	4.72	7061	4295	15408 Hoxb13	4.59	2245	8371
480	107376 E330013P04Rik	4.62	11657	5881	53375 Mtx2	4.72	3125	441	269614 Pank4	4.59	941	7464
481	110052 Dek	4.61	1811	1783	241770 Rims4	4.71	6710	6351	17940 Birc1a	4.59	3358	15629
482	11705 Amh	4.61	379	5751	18208 Ntn1	4.71	27	295	387511 Tas2r134	4.58	602	13571
483	14012 Eva1	4.61	6562	5757	22637 Zap70	4.71	9407	3773	66489 Rp135	4.57	16191	14833
484	66082 Abhd6	4.61	12056	5761	170813 Ms4a3	4.70	1828	16069	70601 Ecd	4.56	9084	3066
485	244187 Olfr684	4.61	8165	7460	244234 5830411N06Rik	4.70	8040	16070	67465 Sf3a1	4.56	6839	6695
486	68606 Pppm1f	4.61	5225	11373	12797 Cnn1	4.70	511	16071	74600 Mrpl47	4.56	9085	13115
487	245386 6430550H21Rik	4.61	82	380	74761 Mxra8	4.70	2456	3648	16852 Lgals1	4.56	2016	544
488	12561 Cd4	4.61	5081	18313	57277 Slrpl1	4.70	6141	16800	11363 Acadl	4.56	2671	17204
489	69104 39512	4.60	6256	1212	66469 2810405K02Rik	4.70	7497	6560	14221 Fjx1	4.55	2829	5011
490	320869 4732415M23Rik	4.60	323	2135	14787 Rhpnl	4.70	4009	8424	57294 Rps27	4.55	3100	4698
491	103172 Ndg2	4.60	6245	2606	80891 Msr2	4.70	6127	1925	26433 Plod3	4.53	100	200
492	14904 Gtpbp1	4.60	2241	14408	217364 D230014K01Rik	4.70	7493	1926	326620 His1t1hb	4.53	4544	749
493	69456 Commd10	4.59	4715	2096	74840 Armet	4.70	377	2130	50723 Icosl	4.53	880	1506
494	19309 Pygm	4.59	6028	8769	14233 Foxi1	4.70	546	1436	13424 Dyncl1h	4.52	7144	2984
495	229474 6330505N24Rik	4.59	3322	2740	22163 Tnfrsf4	4.70	921	8790	269019 Stk32a	4.52	2149	42
496	20168 Rtn3	4.59	1345	9420	104099 Itga9	4.70	4545	4210	67109 Zfp787	4.52	4293	1090
497	23942 Mta2	4.58	5119	10439	280668 Adam1a	4.69	16085	1790	69185 Dtwd1	4.52	7576	3371
498	216961 Centa2	4.58	526	84	64918 Bhmt2	4.69	4222	5528	114863 Prosc	4.52	5251	5474
499	320634 Ocr1	4.57	16257	985	19014 Pparbp	4.69	698	12268	93694 Clec2d	4.51	5666	1632
500	72961 Slc17a7	4.57	11774	1606	232080 Rbed1	4.69	1116	12269	258610 Olfr307	4.51	4440	7568
501	18641 Pfkl	4.56	14490	2948	72354 Ttc4	4.69	1127	6410	272636 D9Ertd280e	4.50	4319	2485
502	14527 Gcgr	4.56	405	9739	15563 Htr5a	4.69	3946	9240	18640 Pfkfb2	4.50	1751	1861
503	67958 2610101N10Rik	4.56	6961	3161	217140 Scrn2	4.69	13309	11282	258700 Olfr1451	4.50	15882	16491
504	22337 Vdr	4.56	91	272	216198 Tcp112	4.67	6318	3107	242585 Slc35d1	4.49	2190	4348
505	18082 Nipsnap1	4.56	3974	179	241196 Serpinb13	4.67	10712	13632	66812 Ppcdc	4.49	7632	6888
506	16913 Psmb8	4.55	1385	1306	17904 Myl6	4.67	11497	5782	171171 Ntnq2	4.49	1972	633
507	19725 Rfx2	4.54	919	872	11431 Acp1	4.67	5375	9419	68563 Dpm3	4.49	2598	14913
508	110006 Gusb	4.54	100	3474	67422 Dhdds	4.66	9546	1141	387314 BC023818	4.48	2304	4072
509	23934 Ly6h	4.54	1771	16634	259063 Olfr691	4.66	2516	597	76308 Rab1b	4.48	5231	351
510	15930 Indo	4.54	4396	5154	219134 Tmem46	4.66	3976	4350	269023 Zfp608	4.48	6169	17089
511	12797 Cnn1	4.54	486	16071	56527 Mast1	4.65	7628	10910	15122 Hba-a1	4.48	2661	7620
512	64290 Foxb1	4.53	8981	4119	246079 Defb9	4.65	12515	5037	20729 Spin	4.48	7164	15748
513	12845 Comp	4.52	1897	5859	28042 D5Wsu178e	4.65	962	58	109108 Slc30a9	4.47	3569	1558
514	319665 A430010J10Rik	4.52	3268	7594	58208 Bcl11b	4.65	4551	2349	71602 Myo1e	4.47	5423	4758
515	12398 Cfba2t3h	4.52	586	2172	243382 Ppm1k	4.64	5107	5024	19025 Ppgb	4.47	8014	17341
516	56088 Dscr2	4.52	6956	4795	15214 Hey2	4.63	3837	10308	209111 Sirt7	4.47	7694	4384
517	227357 Espn1	4.52	4627	7612	170483 Grin3b	4.63	1525	18113	93683 Glce	4.47	1725	5561
518	332396 Kcnk18	4.51	400	1438	11606 Agt	4.63	2557	3139	56438 Rbx1	4.46	2748	3024
519	22187 Ubpb	4.51	4287	2570	14470 Rabac1	4.63	2560	5831	207473 AF529169	4.46	8539	3855
520	319165 Hist1h2ad	4.51	1342	1009	13875 Erf	4.63	39	133	14538 Gcnt2	4.46	1414	6369
521	66717 Ccdc96	4.51	6220	11616	142980 Tlr3	4.63	2548	4406	227998 4933409G03Rik	4.46	18617	7780
522	67859 231002J15Rik	4.50	2790	7375	226693 Ifi205	4.62	2969	3435	69961 2810432D09Rik	4.46	297	9451
523	78777 2410002B10Rik	4.50	7858	207	70979 4931417G12Rik	4.61	3989	13299	114643 Oas1c	4.45	7997	757
524	30841 Fbx10	4.50	13934	4347	14858 Gsta2	4.61	929	14787	54402 Stk19	4.45	217	5779
525	245026 E330026B02Rik	4.50	5031	1509	12323 Camk2b	4.61	8265	1174	52683 D15Ertd785e	4.45	3954	12139
526	76846 Rps9s	4.50	1704	7094	216991 Centa2	4.60	498	84	66855 Tcf25	4.45	9260	2075
527	14300 Rfg1	4.50	3327	456	56774 Slc6a14	4.60	7932	8973	381155 9630014M24Rik	4.45	5204	4741
528	218973 Wdh1d	4.49	11998	245	66775 Ptplad2	4.58	3301	333	319480 Itga11	4.44	6437	1544
529	58172 Sertad2	4.49	960	2176	71738 Mamdc2	4.58	154	170	108013 Brunol4	4.44	1201	476
530	22701 Zfp141	4.49	3765	18114	338374 I2b8	4.58	1977	3792	13048 Cutl2	4.44	342	1920
531	67647 493052C07Rik	4.49	3758	918	19207 Ptc2	4.58	6355	3793	68172 4930517K11Rik	4.43	5616	10762
532	18034 Nfkb2	4.47	4335	617	100434 Slc44a1	4.58	2645	2062	18674 Slc25a3	4.43	3603	16600
533	78709 C630041L24Rik	4.47	1824	13428	11551 Adra2a	4.58	5729	18489	24084 Tek2	4.42	6490	2716
534	75475 Oplah	4.47	3345	762	76157 Slc35d3	4.58	4791	8996	330817 Dhbps	4.42	1777	3520
535	54712 Plxnc1	4.47	886	1428	17152 Mak	4.57	8775	2475	15245 Hrip	4.42	1348	3521
536	230459 Cyp213	4.47	15287	2187	66296 Cep27	4.57	2066	10945	213649 Arhgef19	4.42	445	5633
537	67300 Cltc	4.46	2939	1176	70202 2310051M13Rik	4.57	8254	1070	53978 Edg4	4.41	295	7730
538	69675 Pxdn	4.46	10839	8220	15957 Ifit1	4.56	7140	11653	16192 Il5ra	4.41	4475	11590
539	20016 Rpo1-1	4.46	198	3749	12394 Runx1	4.56	1052	1054	230784 Sesn2	4.41	892	5222
540	230752 2610027C15Rik	4.46	108	7070	66885 Acadsb	4.56	3058	5670	215653 Rassf2	4.41	2402	18487
541	73072 BC068157	4.46	5092	4316	22276 Uros	4.56	4394	12406	18742 Pitx3	4.41	202	9
542	59289 Ccbp2	4.46	1451	243	12581 Cdkn2d	4.56	1224	466	17874 Myd88	4.40	86	5822
543	208169 Slc9a10	4.46	10293	1375	76872 Ccdc116	4.55	1522	5162	16639 Pfkfb1	4.40	3728	14240
544	230935 Dnajc11	4.46	567	4612	16852 Lgals1	4.55	2016	487	17918 Myo5a	4.40	10158	13738
545	50518 a	4.46	4496	15622	20355 Sema4f	4.55	6405	2843	69902 2610012O22Rik	4.39	3864	3257
546	14233 Foxi1	4.45	494	1436	76273 Ndfip2	4.55	6406	2844	320633 Zbtb26	4.39	7131	3259
547	16706 Ksr1	4.44	1331	204	18181 Nrf1	4.55	1559	1333	67134 Nol5a	4.39	2250	2890
548	200188 Map6d1	4.44	7204	6522	320974 B430119L13Rik	4.55	102	233	100213 Rusc2	4.39	11289	2896
549	19130 Prox1	4.44	8580	4886	58212 2900083I11Rik	4.55	15638	7593	56294 Ptpn9	4.37	9045	3387
550	16326 Inhbe	4.44	4790	334	14154 Fem1a	4.55	181	1334	11500 Adam7	4.37	2170	6920
551	228839 Tgif2	4.43	883	9006	227683 Coq4	4.54	1430	5200	76758 Gsdm2	4.37	9730	2647
552	56486 Gabarap	4.43	16406	3173	67087 Ctnnbip1	4.54	1976	7092	231798 Lrch4	4.37	4536	1191
553	214901 Cht18	4.41	13	2896	382913 Neil2	4.53	1024	462	70564 5730469M10Rik	4.37	3021	4529
554	319188 Hist1h2bp	4.41	7219	13457	11629 Al�1	4.53	1965	3070	14622 Gjb5	4.37	6618	5718
555	14472 Gbx2	4.41	12809	6774	19354 Rac2	4.52	8866	691	380686 1500041B16Rik	4.37	6619	8737
556	108153 Adams7	4.41	7256	644	100929 Tyw1	4.51	9827	9074	18478 Pah	4.36	7721	5293
557	67452 Pnplab	4.41	17037	646	234371 Tmem161a	4.50	2786	154	107702 Rnh1	4.36	238	53
558	66508 240001E08Rik	4.41</td										

574	70612 5730494N06Rik	4.37	9172	934	11513 Adcy7	4.46	5256	14721	170711 Otud7a	4.32	5569	6583
575	170735 Arr3	4.37	4471	2709	14599 Gh	4.46	6302	11669	69207 Sfrs11	4.32	3168	16481
576	30853 Mif2	4.37	2582	3686	78816 Gmip	4.46	93	895	20877 Aurkb	4.32	4665	2185
577	16560 Kif1a	4.37	595	17860	20904 Strm	4.46	12371	10974	66383 Nifun	4.31	15745	14340
578	217038 Mrrm1	4.37	5560	17866	22413 Wnt2	4.45	1020	102	27981 D4Wsu53e	4.31	270	3204
579	14555 Gpd1	4.37	937	4523	217369 Uts2r	4.45	3495	6797	258559 Olfr830	4.30	17123	15964
580	22067 Trpc5	4.37	6636	5727	104401 Pcnxl3	4.45	3968	5468	67657 Rabl3	4.30	12835	7616
581	23887 Ggtla1	4.37	1630	8916	64931 Foir4	4.44	7570	13507	53376 Usp2	4.29	1585	6628
582	497106 Rnase12	4.36	9961	9999	77034 2510039018Rik	4.44	11913	3160	17882 Myh2	4.29	9159	8091
583	21957 Tnnt3	4.36	254	61	26396 Map2k2	4.44	16475	4545	14619 Gjb2	4.29	2027	18558
584	212541 Rho	4.36	2224	10044	16821 Lcn4	4.44	1692	17827	66626 5730403B10Rik	4.29	3846	2750
585	56078 Car5b	4.36	1682	309	18753 Prkcd	4.43	4208	905	68859 1190007F08Rik	4.29	6784	12988
586	69550 Bst2	4.36	8727	1893	12398 Cbfaf23h	4.43	515	2172	103784 Al553587	4.28	5460	2225
587	67674 0610038D11Rik	4.35	130	1855	71670 Acy3	4.43	1397	11012	16563 Kif2a	4.28	7317	7090
588	330361 AW146020	4.35	2969	4467	71986 Ddx28	4.43	3221	222	210922 Aytl2	4.28	790	343
589	214917 BC008155	4.35	8568	16312	18392 Orc1l	4.43	8595	5817	258335 Olfr374	4.27	423	431
590	27055 Fkbp9	4.34	9446	1007	382056 Crtc1	4.43	1099	5330	26896 Crsp2	4.27	4870	913
591	230908 Tardbp	4.34	9443	2268	76898 B3gat1	4.41	1419	7623	258067 Olfr1359	4.27	2044	2157
592	108159 Ubxd10	4.34	15444	4816	81907 Tmem108	4.41	15850	917	225870 Rin1	4.27	2614	2755
593	20826 Nhfp21	4.34	2067	748	56857 Slc37a2	4.41	2227	9685	18828 Plscr2	4.27	9217	3505
594	76804 Jmjdc2c	4.34	9229	6655	12770 Ccr11	4.41	993	1987	30928 Zfp238	4.27	285	1362
595	233836 Slc5a11	4.34	9223	10653	16560 Kif1a	4.41	577	17860	64339 Fndc4	4.27	1364	4314
596	403201 5330416C01Rik	4.34	4507	16879	236690 Nyx	4.40	10741	9833	26431 Git2	4.27	8650	14392
597	381306 BC055324	4.34	8586	3182	114141 Cldn16	4.40	11958	15048	259063 Olfr691	4.27	2516	509
598	69051 Pycr2	4.34	9849	11178	14240 Foxb2	4.40	17749	10043	78783 Brpf1	4.27	2517	4690
599	18542 Pcolce	4.34	2304	14293	73032 Ttc9b	4.40	9630	7019	232599 B930018B01	4.27	299	7272
600	17082 II1f1	4.33	4457	1403	21679 Tead4	4.39	2116	6908	27494 Amot	4.26	11655	12568
601	17846 Commd1	4.33	12899	2343	66771 4933439F18Rik	4.39	2112	1124	76407 Spag4l	4.25	8105	172
602	387511 Tas2r134	4.32	13571	482	227631 Sohlh1	4.39	258	384	15512 Hspa2	4.25	6370	15236
603	73453 1700067K01Rik	4.32	3107	1276	52150 Kcnk6	4.38	13956	11779	16597 Klf12	4.25	9952	3081
604	66540 3110001A13Rik	4.32	4943	6752	21406 Tcf12	4.38	6439	14500	666279 Dspp	4.25	1865	8011
605	58210 Sectm1b	4.31	710	1115	240119 St6gal	4.38	8762	18332	83453 Chrd1	4.25	13244	14847
606	218440 6430502M16Rik	4.31	8182	16114	18846 Plxna3	4.37	13971	2436	226976 4632411B12Rik	4.25	4830	3280
607	78304 Lsmd1	4.31	28	652	17433 Mobp	4.37	3745	839	84506 Hamp1	4.24	12635	3762
608	26556 Homer1	4.31	58	11524	219249 Tdrd3	4.37	3746	840	78787 Uspp54	4.24	12636	5919
609	76491 Abhd14b	4.31	11547	11533	56043 Akr1e1	4.37	4525	3054	14376 Ganab	4.24	630	1317
610	104457 0610010K14Rik	4.31	14868	2886	17086 Ncr1	4.37	12487	11070	21427 Vps72	4.23	5544	1448
611	233081 Ffar1	4.31	4447	9777	66061 0610012D17Rik	4.36	778	6491	433004 B830017H08Rik	4.22	8053	6755
612	70747 Tspan2	4.31	5845	335	75671 Tex22	4.36	10687	18731	214854 Linrc	4.22	124	131
613	114615 Elac1	4.31	5843	472	69113 Alkbh3	4.36	1599	1975	268980 Strm	4.22	4850	8073
614	26891 Cops4	4.31	3517	682	277414 Trp53i1	4.36	3677	1466	20310 Cxcl2	4.22	9098	4190
615	70097 Sash1	4.31	4563	6690	229714 Gpr61	4.36	265	2754	71685 Galnt14	4.22	6695	6293
616	67338 Rff1	4.31	6424	9199	16330 Inpp5b	4.36	5303	4266	72236 Tsnarip1	4.22	12893	4852
617	319503 9930038B18Rik	4.31	5102	17465	18601 Pad3	4.36	6292	992	18034 Nfkb2	4.22	532	4335
618	71276 Ccdc57	4.30	16009	15808	23875 Gpr150	4.36	13178	5484	22410 Wnt10b	4.22	14225	9024
619	228368 Slc35c1	4.30	4119	289	15248 Hic1	4.36	855	3279	18986 Pou2f1	4.22	9650	2942
620	68303 9130005N14Rik	4.30	2156	1024	214951 Rhbd1	4.34	8235	17284	83602 Gtf2a1	4.21	14279	9261
621	210444 Adcy2	4.29	6752	7389	382571 Kcnf1	4.34	15155	17285	27367 Rp13	4.21	9990	15284
622	102209 Snapc2	4.29	4910	5099	71514 Stpq	4.34	1735	3087	27388 Ptddss2	4.20	649	2627
623	192166 Sardh	4.28	8693	1061	17827 Mtx1	4.34	398	15	67166 Arl8b	4.20	3080	4775
624	258095 Olfr119	4.27	11312	702	21428 Mix	4.34	1226	8198	12995 Csnk2a1	4.20	1672	8057
625	11674 Aldoa	4.27	1893	6853	11841 Arl2	4.34	5849	3449	74646 Spsb1	4.20	8113	1711
626	13167 Dbi	4.27	1161	1439	114893 Dcu1d1	4.34	3798	3450	73251 Setd7	4.20	7173	8123
627	67867 Lrrcc2	4.27	8843	47	403174 A930005I04Rik	4.34	1957	18733	19076 Prim2	4.20	8556	9997
628	320208 A830041P22Rik	4.27	768	2918	18566 Pdcod1	4.33	10759	17949	68149 Outub2	4.19	994	7205
629	18424 Otx2	4.27	9437	5612	59126 Nek6	4.33	12338	9820	17898 Myl7	4.18	3475	23
630	14376 Ganab	4.27	1317	609	22346 Vh1h	4.33	3043	6536	18510 Pax8	4.18	144	447
631	170770 Bbc3	4.27	6224	7423	109575 Tbx10	4.33	6523	8778	17313 Mgp	4.18	4074	742
632	109006 Clapin1	4.26	12200	5349	192169 1810047C23Rik	4.32	13349	11817	20347 Sema3b	4.18	1034	743
633	280287 Kiss1	4.26	3598	1146	171171 Ntng2	4.32	1972	506	23010 Blvr	4.18	67	2320
634	228357 Lrp4	4.25	18123	6267	227522 Rpp38	4.31	3035	10545	94353 Hmgm3	4.18	1989	7220
635	23957 Nr0b2	4.25	6004	2388	140493 Kcn3	4.31	893	10546	21846 Tie1	4.18	4133	13647
636	227693 Zyg11bl	4.25	14365	7690	107700 Tm6sf2	4.31	15239	18391	23832 Xcr1	4.18	3998	15342
637	22902 Tsga2	4.24	366	1765	193043 Trpv1	4.31	4465	15783	258283 Olfr981	4.18	6521	15347
638	11883 Arsa	4.24	2382	2373	70292 2600003E23Rik	4.30	1398	281	21483 BC021381	4.17	6272	657
639	58193 Ext2	4.24	13832	4723	13350 Dgat1	4.30	2369	4869	100756 Usp30	4.17	468	8137
640	211548 Nomo1	4.24	2466	13660	209683 Ttc28	4.30	3094	4542	67685 Dyx1c1	4.17	13157	16164
641	67198 281002L20Rik	4.24	6281	137	230654 Lrrc41	4.29	667	1188	17386 Mmp13	4.17	1951	6552
642	67037 Pmrf1	4.24	1458	3231	67131 Acbd4	4.29	989	13704	66594 Ugcr	4.17	3335	402
643	381409 Cdhd26	4.24	806	4186	105734 Tigd5	4.29	2255	7035	140474 493340511Rik	4.17	4056	13386
644	72318 Pscd4	4.24	4037	4189	14148 Fdx1	4.29	4969	15872	108153 Adams7	4.16	556	7256
645	15944 Irgm	4.24	2481	6880	103655 Sec14l4	4.29	4966	9671	26445 Psmb2	4.16	10645	9140
646	21853 Timeless	4.24	17213	348	26926 Pdcdb2	4.29	388	79	67452 Pnplab	4.16	557	17037
647	13626 Eed	4.24	14345	1458	64294 Itm2c	4.28	1017	3151	15414 Hoxb6	4.16	925	2779
648	54485 Dil4	4.24	2574	572	22318 Vamp2	4.28	1018	7210	74470 4933440J22Rik	4.14	1510	141
649	27388 Ptdss2	4.23	2627	622	72026 Trmu	4.28	397	18040	16163 Il13	4.14	1981	1832
650	13805 Eng	4.23	2165	4908	228136 Zdhhc5	4.28	725	2569	72148 2610019F03Rik	4.14	7285	8220
651	269855 A430110N23Rik	4.22	10608	9	257900 Olfr1024	4.28	3895	16681	234912 9230110C19Rik	4.14	12142	15380
652	50701 Ela2	4.22	1547	4954	192662 Arhgdia	4.28	5963	16682	78304 Lsmd1	4.14	607	28
653	22441 Xlr	4.22	9601	6820	56174 Nagk	4.28	4612	1088	8093 Fgf16	4.14	1759	214

670	65107 Lrp10	4.18	1217	1327	233424 Trmc3	4.22	12326	1321	59012 Moxd1	4.10	1297	3108
671	20220 Sap18	4.18	5058	4392	66177 Ubl5	4.21	11748	10537	53415 Htatip2	4.10	6067	4949
672	12798 Cnn2	4.18	2604	6152	217700 4632408A20Rik	4.21	3203	1596	403186 B93001P16Rik	4.09	886	2947
673	19763 Ring1	4.18	5698	205	207728 Pde2a	4.21	2056	18679	53902 Dscr1l2	4.09	1558	284
674	16419 Itgb5	4.18	3655	1500	110696 H2-M10.3	4.21	12890	16798	72565 Uaca	4.09	228	2506
675	15374 Hn1	4.18	785	3906	67978 4432405B04Rik	4.20	1079	11283	381373 Sp9	4.08	3019	815
676	59095 Fxyd6	4.18	6036	10836	235312 C1qtnf5	4.20	8173	18087	20682 Sox9	4.08	10745	10987
677	70466 Ckap2l	4.17	3673	6413	259172 Mfrp	4.20	8174	18088	16210 Impact	4.08	1827	2057
678	231605 Galnt9	4.17	35	8077	110902 Chrn2	4.20	3182	12124	68792 Srp2x	4.08	5243	2799
679	64058 Perp	4.16	1998	3304	11811 Apobec2	4.20	1948	12125	104570 AW011752	4.08	1328	13153
680	19013 Ppara	4.16	3289	3306	68203 Diras2	4.20	5737	18089	13006 Smc3	4.08	5244	16297
681	13367 Diap1	4.16	2003	7008	20382 Sfrs2	4.19	1596	4888	242523 Dmrt1	4.08	810	2625
682	331026 Gmppb	4.16	348	15732	13209 Ddx6	4.19	960	16	26891 Cops4	4.08	614	3517
683	12577 Cdkn1c	4.16	5708	2883	110524 Dgkq	4.19	2416	5684	56318 Acpp	4.08	2570	5839
684	18546 Pcp4	4.15	1409	4121	17926 Myoc	4.19	10655	8425	13714 Elk4	4.08	6285	9290
685	404634 H2afy2	4.15	1386	5825	21719 BC025575	4.19	6130	4924	64059 Oxdct2a	4.07	322	338
686	23939 Mapk7	4.14	17348	2117	75570 Nhej1	4.19	4010	13557	217410 Trib2	4.07	14132	3780
687	18241 Gpr143	4.14	2813	5266	22591 Xpc	4.19	2386	6132	67101 2310039H08Rik	4.07	1703	1023
688	235582 6230410P16Rik	4.14	2815	10886	19342 Rab4b	4.19	14479	12810	66706 4733401H18Rik	4.07	14	2996
689	193813 Mcfd2	4.14	13181	2534	68879 Prpf6	4.19	12	9080	76917 2810417J12Rik	4.07	1704	7294
690	52585 Dhrs1	4.14	3141	12975	71711 Mus81	4.19	1149	8091	53325 Bamp	4.07	6734	15487
691	57749 Piwi1	4.14	5882	2152	234378 Klhl26	4.18	1474	1702	19354 Rac2	4.07	8866	555
692	12049 Bcl2l10	4.14	10749	6474	21367 Cntn2	4.18	1970	12200	66526 2210012G02Rik	4.07	1253	12601
693	66168 Grina	4.14	5738	919	19201 PstPIP2	4.17	223	1615	74498 Gorasp1	4.06	1101	11610
694	71538 Fbxo9	4.13	2644	6217	53421 Sec61a1	4.17	836	894	224132 Dirc2	4.06	13048	11616
695	83456 Mov10l1	4.13	3744	6218	210148 Slc30a6	4.17	8568	17537	11838 Arc	4.06	6081	2309
696	192212 Prom2	4.13	663	3190	242509 Bnc2	4.16	10198	2430	68118 9430032L20Rik	4.05	279	1890
697	69683 2310044H10Rik	4.12	1040	11509	171486 Cd99l2	4.16	3941	2041	20357 Sem5b	4.05	1747	7645
698	19014 Pparbp	4.12	499	12268	223917 Krt79	4.16	13615	18479	12447 Ccne1	4.05	3526	9338
699	83491 Pramef1	4.12	2028	1459	11542 170001D09Rik	4.16	9067	659	68498 Tspan11	4.05	10024	13693
700	18817 Plk1	4.12	2768	12452	15211 Hexa	4.16	3239	2704	71943 Tom111	4.05	5172	18387
701	29820 Tnfrsf19	4.11	3740	17176	75612 Gns	4.15	4138	315	213573 Efcb4a	4.05	2626	2665
702	76257 Slc38a3	4.11	4727	1612	20737 Spn	4.15	8034	9880	258095 Olfr119	4.05	624	11312
703	29873 Cspg5	4.11	1275	6505	170458 Gpha2	4.15	2580	2988	114644 Slc13a3	4.05	5218	17170
704	74388 Dpp8	4.11	10982	190	74153 Ube1l	4.15	395	1175	216190 Dip3b	4.05	990	6503
705	252909 V1rr3	4.11	2402	1798	12821 Col17a1	4.15	12668	3896	66266 1810011O16Rik	4.03	3187	3693
706	11495 Adam2	4.11	7063	3478	258379 Olfr1284	4.15	6010	7449	69379 C8g	4.03	7792	5306
707	53334 Gosr1	4.11	7068	3480	74589 4933428M03Rik	4.15	11742	17583	56811 Dkk2	4.03	9809	2394
708	17749 Polr2i	4.11	13955	3486	23885 Gmcl1	4.15	169	5752	12834 Col6a2	4.03	10076	9370
709	53626 Insm1	4.11	4205	764	19213 Ptfl1a	4.14	1712	1920	212518 Spn	4.02	1518	4634
710	77938 A930008G19Rik	4.11	2609	2538	58210 Sectm1b	4.14	605	1115	84652 Drctnb1a	4.02	244	54
711	53607 Snrpa	4.10	95	655	225392 4631403P03Rik	4.14	4672	4961	30590 9430071P14Rik	4.02	2150	6830
712	24074 Taf7	4.10	5799	1749	105847 Tmem153	4.14	2420	1302	217869 Elif5	4.02	8949	15311
713	17423 Ndst2	4.10	9747	2526	56368 Cyb561d2	4.14	2422	10036	75430 3200002M19Rik	4.01	3350	2856
714	69009 Thap7	4.10	762	3640	54217 Rpl36	4.14	1785	3503	52004 Cdk2ap2	4.01	6593	3845
715	73712 Dmkn	4.09	2532	953	22658 Pgcf2	4.14	1250	127	13870 Erc1	4.01	5328	10539
716	235584 Dusp7	4.09	2535	4572	58865 Tdh	4.14	1783	1649	22130 Ttf1	4.01	9784	10541
717	18823 Plp1	4.09	15222	189	72572 Spats2	4.14	14761	2395	232854 Zfp418	4.01	2324	14700
718	13090 Cyp2b19	4.09	381	11108	239559 A4gal	4.13	3290	8534	67073 Pt4k2b	4.01	1318	1708
719	225164 Mib1	4.09	11500	11117	230738 Zch3h12a	4.13	4109	6649	380712 2010305C02Rik	4.01	2930	1106
720	73991 Spg3a	4.08	13269	54	67464 Entpd4	4.13	18549	15325	75516 Ttc32	4.01	4360	18427
721	12552 Cdh11	4.08	5295	218	442809 4932416K20Rik	4.12	1871	12541	13052 Cxadr	4.00	14760	12032
722	140723 Caeng5	4.08	101	2576	13119 Cyp44a14	4.12	2506	2159	108160 D0HXS9928E	3.99	658	2744
723	66043 Atp5d	4.08	16303	5742	19337 Rab33a	4.12	17408	16132	207742 Rnf43	3.99	10999	9423
724	52377 Rcn3	4.08	16887	1843	56873 Lmbr1	4.12	4193	10	12175 Brnp2	3.99	17999	11398
725	228136 Zdhhc5	4.08	650	2569	22350 Vll2	4.12	10731	2766	381314 Lars2	3.98	4428	5382
726	22415 Wnt3	4.07	1011	367	68948 1500011H22Rik	4.11	10520	3112	72503 2610507B11Rik	3.98	772	2145
727	258617 Olfr356	4.07	8408	65	74375 Gcc1	4.10	1212	4135	15483 Hsd1b1b	3.98	6651	5130
728	213053 Slc39a14	4.07	1069	7661	18810 Plec1	4.10	277	5917	236794 Slc9a6	3.98	2343	242
729	67078 1700012G19Rik	4.06	15759	791	18039 Nefl	4.10	1767	14351	110382 C8b	3.98	186	841
730	333670 Gm867	4.06	775	5152	246085 Defb10	4.10	6289	10691	12491 Cd36	3.98	11650	6366
731	14923 Guk1	4.06	1157	15547	56485 Slc2a5	4.10	14593	10692	237029 4932411N23Rik	3.97	10577	5564
732	240614 Ranbp6	4.06	18293	3012	22412 Wnt9b	4.10	3355	10868	73626 1810009J06Rik	3.97	10578	6943
733	74978 Lrrq1	4.05	14604	14425	19280 Ptrps	4.10	1025	2778	242785 Klh21	3.97	159	1114
734	14977 Slc39a7	4.05	6106	188	66433 Chchd7	4.09	6263	3345	257950 Olfr1039	3.97	5366	1538
735	12462 Cct3	4.05	4033	353	71701 Pnpt1	4.09	12866	13913	258578 Olfr1517	3.97	5367	1539
736	66073 Txndc12	4.05	12430	5600	26458 Slc27a2	4.09	2015	4487	21761 Morf41	3.97	9427	14445
737	68977 Hagh1	4.05	4882	17255	70061 Sdro	4.09	18344	17654	67392 4833420G17Rik	3.96	7543	9500
738	66942 Ddx18	4.05	5212	4548	414077 BC056474	4.09	12692	11266	236643 Syt15	3.96	10222	18472
739	66193 1110049F12Rik	4.05	895	15002	63986 Gmfg	4.09	6402	11267	67205 Utp11	3.95	8253	2176
740	72027 Sic39a4	4.05	3811	5784	20521 Slc22a12	4.08	2095	4003	231600 Chfr	3.95	13566	5168
741	258441 Olfr1310	4.04	16946	2605	67573 Lox14	4.08	2097	15404	83672 Syt13	3.95	4349	8509
742	22223 Uchl1	4.04	8467	4654	17313 Mgp	4.07	4074	631	237253 Lrp11	3.95	5453	16463
743	225888 Suv420h1	4.04	6838	17799	20347 Sema3b	4.07	1034	632	53886 Cdk12	3.95	3294	1055
744	66673 Sorcs3	4.04	263	3858	77065 Int5	4.07	14637	12969	192163 Pcdha3	3.95	14234	4316
745	329628 Fat4	4.03	5380	3432	12057 Opn1sw	4.07	1490	5118	320394 Cempt	3.95	1369	4318
746	271047 Serpina3b	4.03	110	7222	214425 Cilp	4.07	917	14594	11813 Apoc2	3.95	2166	12746
747	243725 Ppp19a	4.03	9120	3978	11545 Parp1	4.07	1557	88	72075 Ogfr	3.94	127	1545
748	76405 1700018B08Rik	4.03	112	6626	16499 Kcnab3	4.06	1799	8256	20826 Nhp2i	3.94	593	2067
749	13864 Nr2f6	4.03	9113	6633	326620 Hist1h4b	4.06</td						

Supplemental Material Table 2. Position Weight Matrices for the AHR

Matrices formed using 7 kb upstream and 3 kb downstream of the TSS background							Matrices formed using 2 kb upstream and 2kb downstream of the TSS background						
AHR.DME.10kb							Core 5 NT are: GCGTG						
6 basepair PWM							Matrices in red do not contain 5 NT core.						
P0	A	C	G	T			P0	A	C	G	T		
01	0	0	47	0			01	0	0	25	0		
02	0	0	47	0			02	0	0	25	0		
03	0	47	0	0			03	0	25	0	0		
04	0	0	47	0			04	0	0	25	0		
05	0	0	22	25			05	0	0	0	25		
06	0	0	47	0			06	0	0	25	0		

7 basepair PWM							7 basepair PWM						
P0 A C G T							P0 A C G T						
01	0	0	24	0			01	0	0	22	0		
02	0	0	24	0			02	0	0	22	0		
03	0	0	24	0			03	0	0	22	0		
04	0	24	0	0			04	0	0	22	0		
05	0	0	24	0			05	0	22	0	0		
06	0	0	15	9			06	0	0	22	0		
07	0	0	24	0			07	0	8	14	0		

8 basepair PWM							8 basepair PWM						
P0 A C G T							P0 A C G T						
01	0	0	27	0			01	0	0	19	0		
02	0	0	27	0			02	0	0	19	0		
03	0	0	27	0			03	0	0	19	0		
04	0	0	27	0			04	0	0	19	0		
05	0	16	0	11			05	0	19	0	0		
06	0	0	27	0			06	0	0	19	0		
07	0	0	15	12			07	0	3	11	5		
08	0	0	27	0			08	0	0	19	0		

9 basepair PWM							9 basepair PWM						
P0 A C G T							P0 A C G T						
01	0	25	0	0			01	0	0	20	0		
02	0	15	10	0			02	0	0	20	0		
03	0	25	0	0			03	9	0	11	0		
04	0	25	0	0			04	0	0	8	12		
05	7	9	9	0			05	0	0	20	0		
06	0	25	0	0			06	0	6	0	14		
07	0	12	13	0			07	0	0	20	0		
08	0	25	0	0			08	0	0	0	20		
09	0	25	0	0			09	0	0	20	0		

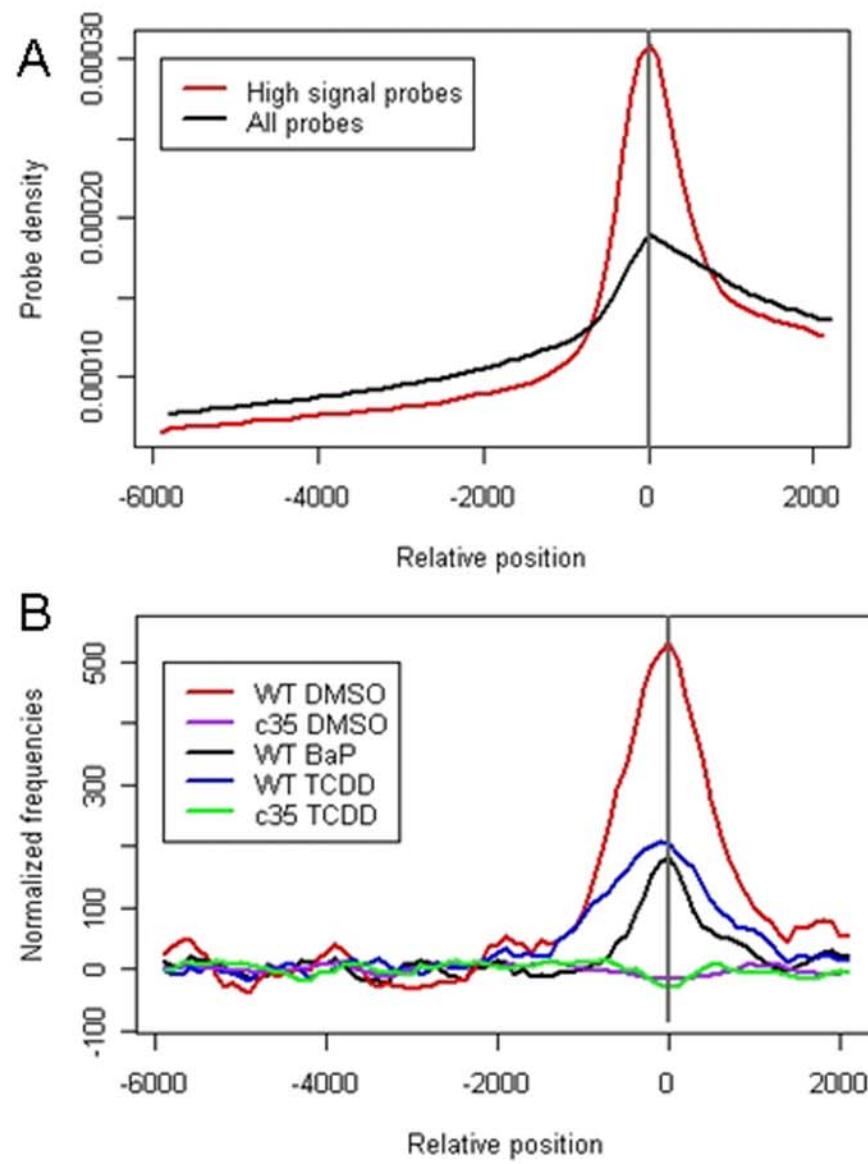
PWM	DMSO Hepa-1		BaP Hepa-1		TCDD - Hepa-1		DMSO c35	
	Mann-Whitney	Fisher's exact	Mann-Whitney	Fisher's exact	Mann-Whitney	Fisher's exact	Mann-Whitney	Fisher's exact
Ahr	8.66E-10	6.37E-08	8.49E-03	8.81E-03	4.70E-05	8.20E-04	0.44	0.37
Ahr.Arnt	2.14E-05	1.78E-03	6.82E-02	5.44E-02	1.71E-06	3.04E-03	0.40	0.29
Ahr.Arnt.HIF1	7.84E-13	5.76E-06	9.16E-03	4.28E-03	1.52E-04	5.01E-03	0.19	0.37
Ahr.DME.4kb	<1.00E-16	1.04E-03	2.54E-05	4.98E-01	1.04E-08	4.37E-02	0.76	0.94
Ahr.DME.10kb	2.22E-16	1.37E-04	9.12E-06	7.91E-01	6.58E-08	1.53E-02	0.71	0.87
PWM	DMSO Hepa-1		BaP Hepa-1		TCDD - Hepa-1		DMSO c35	
	Mann-Whitney	Fisher's exact	Mann-Whitney	Fisher's exact	Mann-Whitney	Fisher's exact	Mann-Whitney	Fisher's exact
Ahr	5.12E-09	3.42E-06	3.58E-02	9.41E-02	2.33E-04	1.12E-02	0.75	0.74
Ahr.Arnt	7.53E-05	6.98E-03	2.13E-01	2.75E-01	1.32E-05	1.91E-02	0.72	0.72
Ahr.Arnt.HIF1	7.51E-12	9.12E-05	3.80E-02	6.05E-02	5.88E-04	2.33E-02	0.56	0.74
Ahr.DME.4kb	<2.20E-15	4.74E-03	2.35E-04	1.00E+00	3.52E-07	9.42E-02	0.88	0.98
Ahr.DME.10kb	4.12E-15	1.01E-03	9.75E-05	1.00E+00	1.05E-06	4.58E-02	0.88	0.96

The values highlighted are the most significant for each comparison test and treatment

Supplemental Material Table 3. PCR primer sets used to validate ChIP/chip data

Gene	Chromosome localization	Coordinates	Primers		Amplicon size (bp)
			Forward	Reverse	
App	16	85172975-85173575	CGTGTGGAGATGGGAAGT	TTTTACCTCCCTGCCTCCTT	117
Itgb5	16	33503850-33504450	GACGAAATGGCCTGACAGAT	GGCCTGCAGAGATTACTTGG	92
Foxo3a	10	42087950-42088550	AATCCCTATCCCACGATCC	CGAGAGGGTTTGTGGAA	128
Hprt1	X	48079702-48080302	ctgcctcgccctccaaatg	AGGCCAGTTCTTCACAAA	104
Foxb1	9	69794735-69795335	CAAGCGCACGTTTCAATA	TCCTCCCTCTGGTTAT	95
Plcd1	9	118771536-118772136	GAGCTGCTCTGGAGGTAC	TACACTGTGGCCAAGCTGAC	78
Gmcl1	6	86808402-86809002	GTGTTGACGGGTTCACT	AAAACAAGGCAGCAGAAGGA	70
Hoxa4	6	52154350-52154950	GGGCTGAAGAAAAGCTCAA	TACCCAGGGTCCCTTATCC	129
Pax4	6	28382050-28382650	CTCAGATTGTCTGGCCATT	GCTCACTTCCAGCACCTAC	71
Jun	4	94445153-94445753	GAGCACGTAAGTGCGTTGAA	TTCCAGGTACAGCACACTGC	113
Wnt4	4	136655425-136656025	CCCCAGGAGAACCCAGT	ggccgaggatgggttac	98
Cyp1b1	17	78010700-78011300	GCTTGGAGACAATTCCAA	AACTCGAGTCACCTGGAGGA	85
Cyr61	3	145550700-145551300	ACCAGAGTTGTCGGGATG	TCCAGTGTGTCCTTGAA	104
Nr2f2	7	66215521-66216121	GGGCTTCTGAGTCCTTACCC	GGAAAGGTATCGGCCTCAT	97
Nr2f2	7	66217062-66217662	AGGGCAGATCAGCACCTAGA	CGGAGTTGCCTCTTC	113
Klf5	14	93699878-93700478	CTCCGGAGACGATCTGAAAC	GCTTACCTGGACCAGCTCCT	97
Lect1	14	74344700-74345300	No acceptable primers		NA
Zic2	14	116879495-116880095	gccCGAGCTCCTTAAATACA	ggaggaggaggtggagga	72
Nr2f1	13	75213762-75214362	CACACACTCGCACACACT	GCTTCCTCATGTCGGCTCA	122
Nr2f1	13	75216700-75217300	GTGCCCTTCTCCAAACCAA	TCGTTTCCCCAGTACCATC	87
Pik3r1	13	47393100-47393700	ACCACTCCTGCCTCGTCACT	CGTGTGACATGTAGGCTCTCA	79
Avp	2	130326600-130327200	GAGAGGGCACAACTCGAAG	atacagaGGCACCCAAGCAC	83
Cdh4	2	179944000-179944600	GAGACCGAGTGGCTGAAC	CCTGGTCATCGCAGAGAAT	90
Tgif2	2	156579276-156579876	CAAAGGTCTGCGCTGGAAAT	ATTGCCAGAACCTCTTTT	101
Tgif2	2	156581000-156581600	AAAGCTCCAAAGCTCCCT	GCAACGTGCACTTTGAAAC	98
Foxg1	12	47393100-47393700	GGCTCTAGGGAAGGGAGACT	CAGGACGGTTGTGACCTCT	108
Foxg1	12	47395140-47395740	AGCCATTATAAGCGGTGGTG	tcccttctcccccttca	120
Tieg3	12	22487150-22487750	GGTACATGTCGAGTGGCTGA	TTGGGTTAGGGACGACATC	122
Esrrg	1	187524167-187524767	TGAGGCAGCTCTGTGACTGT	GCGCCTATTCTTAGCACCTG	74
Gbx2	1	89834873-89835473	GGTAGCCGGTGTAGACGAAA	CGCCTTCAGCATAGACTCG	74
Prox1	1	189706178-189706778	AGGGTATTCCCTGCCCTAGA	GCTCCGCACCATCTGTTAAT	118
Npas4	19	4884200-4884800	AGCGGCAGTTAGCACATT	CTTCTTGCTGGAGGTGAGC	96
Pten	19	32455540-32456140	GAAGCACTGCAATCTGACCA	GTCTGCCCCGCTGTTCTTC	70
Foxc2	8	119749202-119749802	GTTCATGTTGGTGCATCCT	TTCTGGCTCAAAGGAGTTT	102
Hhip	8	78601604-78602204	GGAAGGAACAGCGATTTTGAA	AATCCTTGGACACACCAAGC	110
Fgfcr3	5	32784100-32784700	TCCTGGAACTGTCAGGCTT	GGCTCAGAAGGTTGACTTCG	130
Flt1	5	146620344-146620944	AGGTTCAGGGCTCTGCTCT	GGGAGCTGGTAAGGATTTC	80
Slit2	5	47312722-47313322	GGGGCTGCTAAAGGAGTT	TGTTGTAGGGAGGTGCGAG	89
Aldh3a1	11	61289128-61289728	AAACAGTGGGTGGGTGAGAG	GACATGAGTCACCATCG	102
Ebf1	11	44570176-44570776	CTTGATAGTGGCTGGCTTC	ACAAAGCGCTTAAGCTCAA	107
Hoxb13	11	96298934-96299534	AACTGGCTTGACCTCCCT	CAAATGCACTGAAAGCCTCA	73
Hoxb13	11	96304250-96304850	AGTTGGAGGAGTGGCTGAA	CTCACACAGGAGTCTGCAA	104
Hoxb7	11	96394700-96395300	TTTCCTGGACTCAGGTTGG	GTCCCAGAGAGGGAGGTAG	71
Mapk7	11	61575450-61576050	TTGGGATTCCCTGAGTCTTG	CCGCGGTTCTGTTAAGTGA	72
Ntn1	11	68466542-68467142	GCGAGTTGTCGAAGTCGTG	TCACCAACAGAACGAGCAG	129
Ntn1	11	68468706-68469306	CTTTCTTCGCAGAGGTCCA	CTTTCCAGTTCCCTTCCCT	122
Sertad2	11	20494422-20495022	CGTCCTTGCTCCTGAAATC	CGATTCCGGAGTGGATAAGGAT	103
Supt4h1	11	87806360-87806960	CGCAATCGAGAGGCTTTAG	CCCAGGAATGCTAGCTTGAG	100
Wnt9a	11	59386294-59386894	TACCTTGTCGAAGCATGAGC	GCTCCGGAAGTAAGGGTAGC	112
Wnt9a	11	59387372-59387972	GGGCTTCACACAGACCAGT	AGGGACCTCATACCCAAAC	78

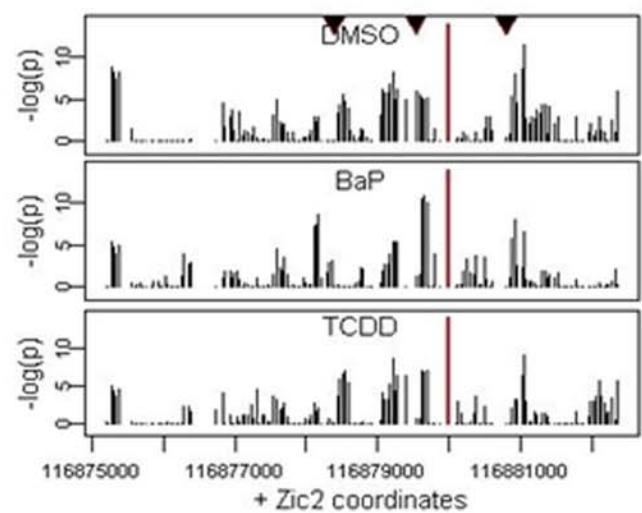
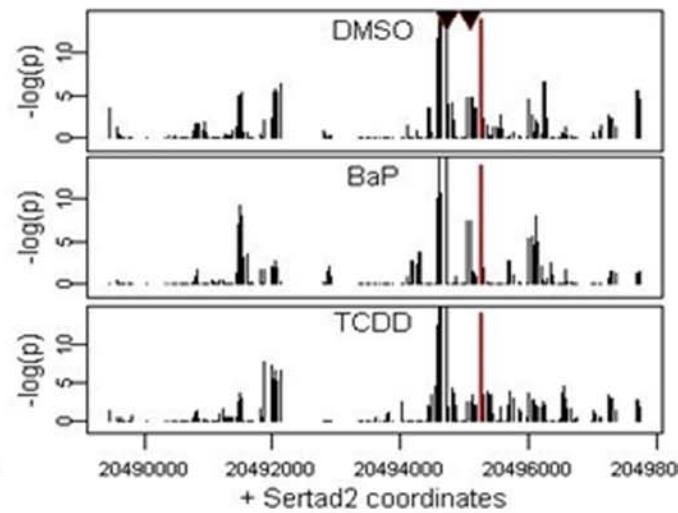
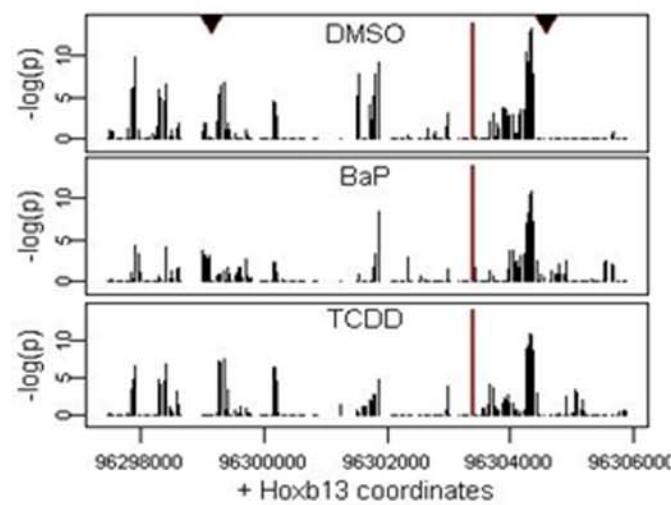
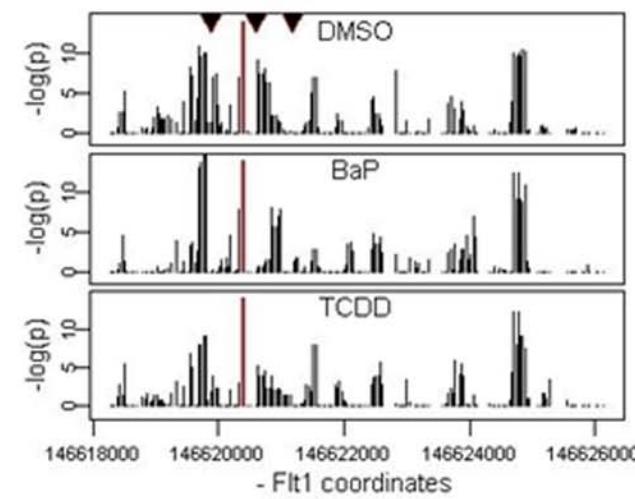
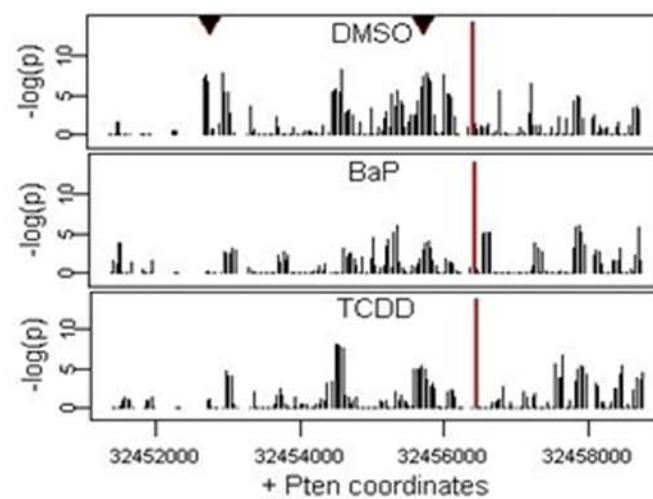
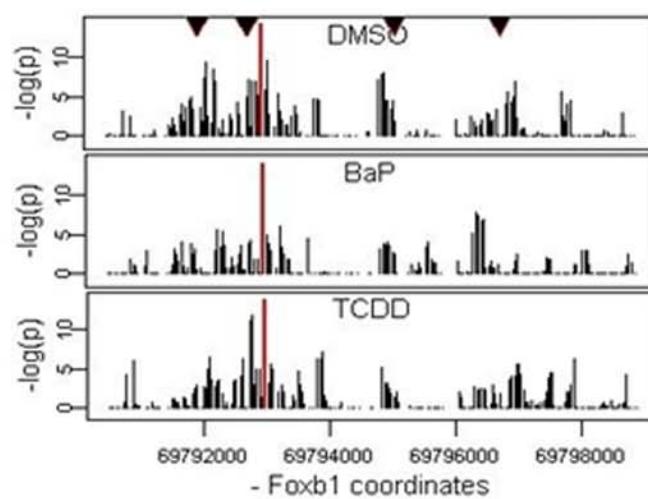
Supplemental Material Figure 1. Analysis of AHR binding sites in gene promoters. **(A)** The curves show the position of all probes in the Affymetrix GeneChip Mouse Promoter 1.0R Array relative to known gene transcription start sites as well as the relative position of the top-ranked 15% high-signal probes. **(B)** The curves show the position of regions of significant probe detection relative to known gene transcription start sites, after accounting for an approximate 8-fold difference in variance between probes along the entire range of hybridization signals. There is a high frequency of regions with significant detection levels within 1kb of the gene start sites in naïve (DMSO), BaP-, and TCDD-treated wild type cells, whereas there is no trend for c35 cells following either vehicle or TCDD treatment.



Supplemental Material Fig. 1

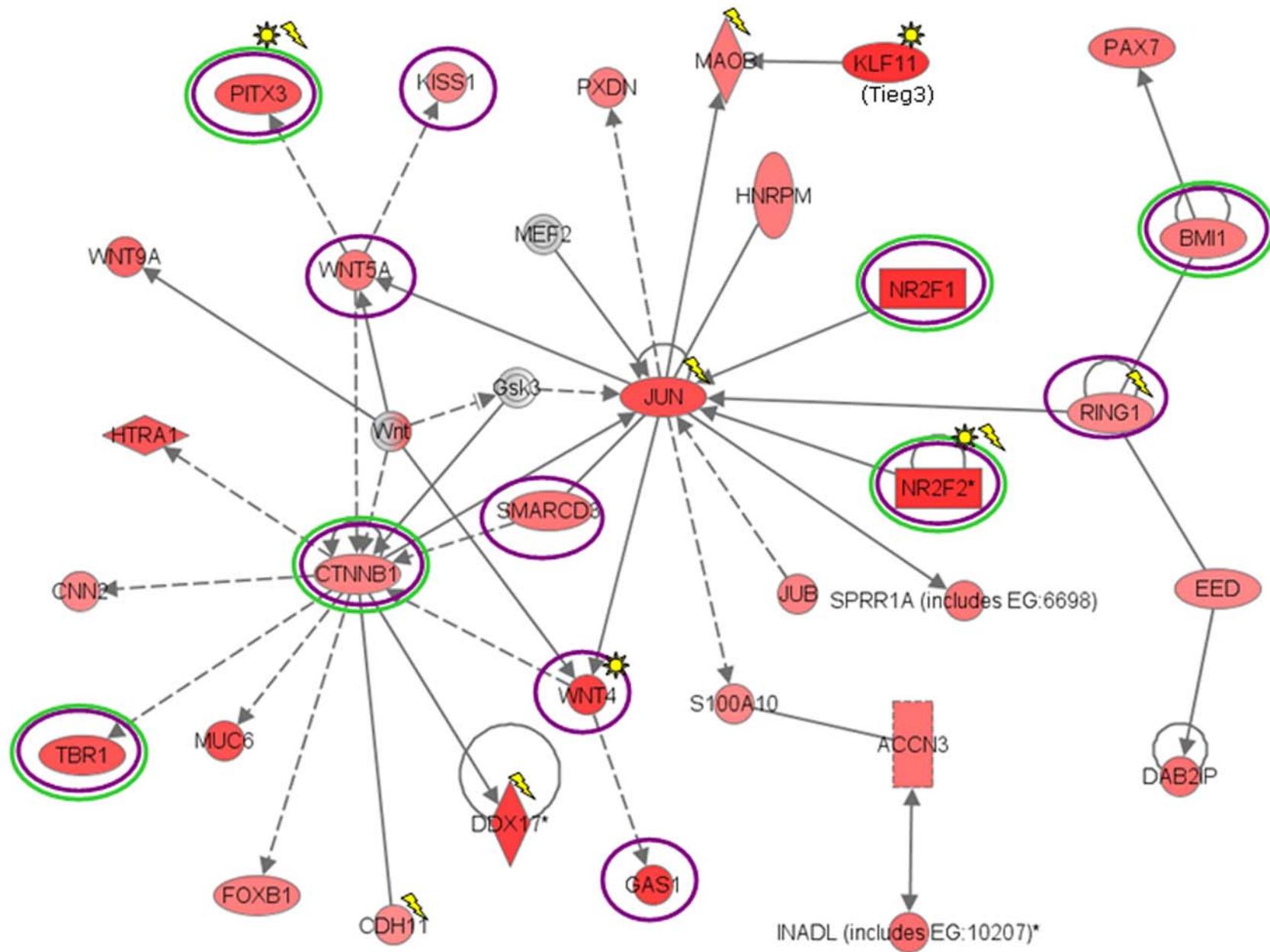
Supplemental Material Figure 2. Differential AHR binding profiles for a selected group of genes chosen from among the top 750 ranked genes.

Three profiles displaying $-\log(p)$ of the comparison of anti-AHR immunoprecipitation to control with non-immune IgG are shown for each gene as a function of promoter coordinates. The profiles correspond to AHR binding targets in naïve, DMSO-treated cells; AHR binding targets in BaP-treated cells; and AHR binding targets in TCDD-treated cells. The *inverted triangle* indicates the sequence-predicted AHR binding sites, based on the 5-nucleotide motif. For each gene, three profiles displaying $-\log(p)$ as a function of promoter coordinates are shown relative to control immunoprecipitation with non-immune IgG, including: (i), AHR binding targets in naïve, DMSO-treated cells ; (ii) AHR binding targets in BaP-treated cells; and, (iii) AHR binding targets in TCDD-treated cells. Location of the sequence-predicted AHR binding sites, based on the 5-nucleotide motif is indicated. The *vertical bar* denotes the position of the TSS. The *positive* or *negative signs* in the abscissa indicate the direction of transcription for each gene, from left to right if *positive*, and the reverse if *negative*.



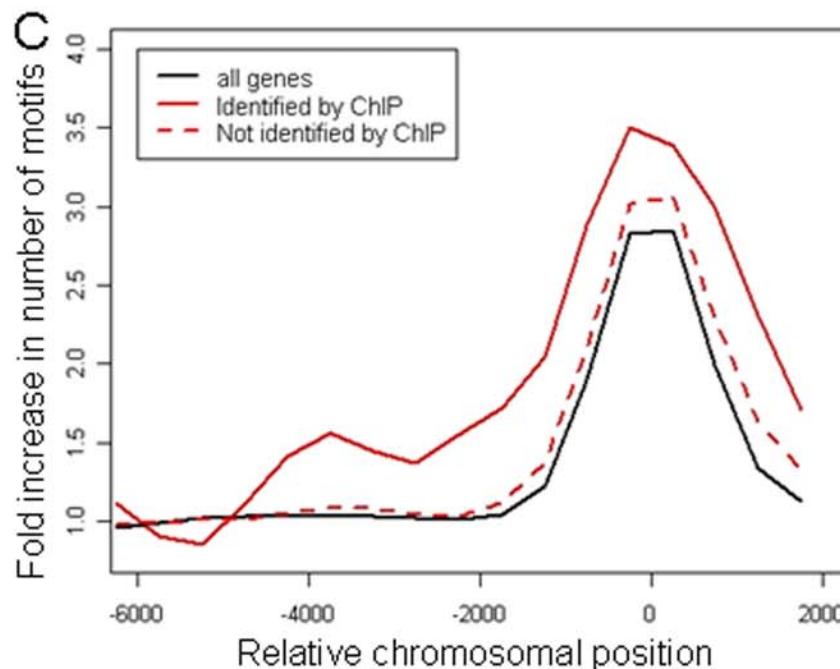
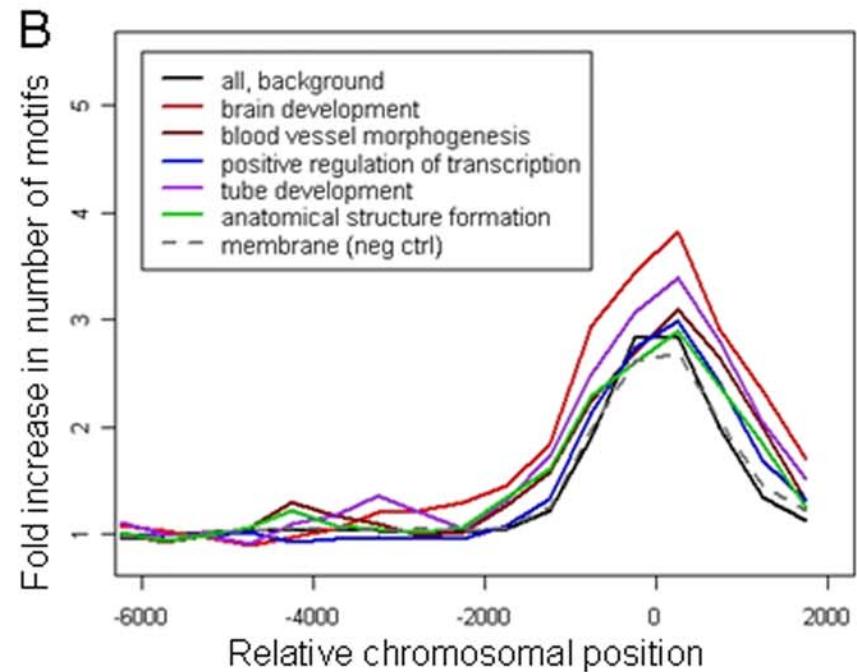
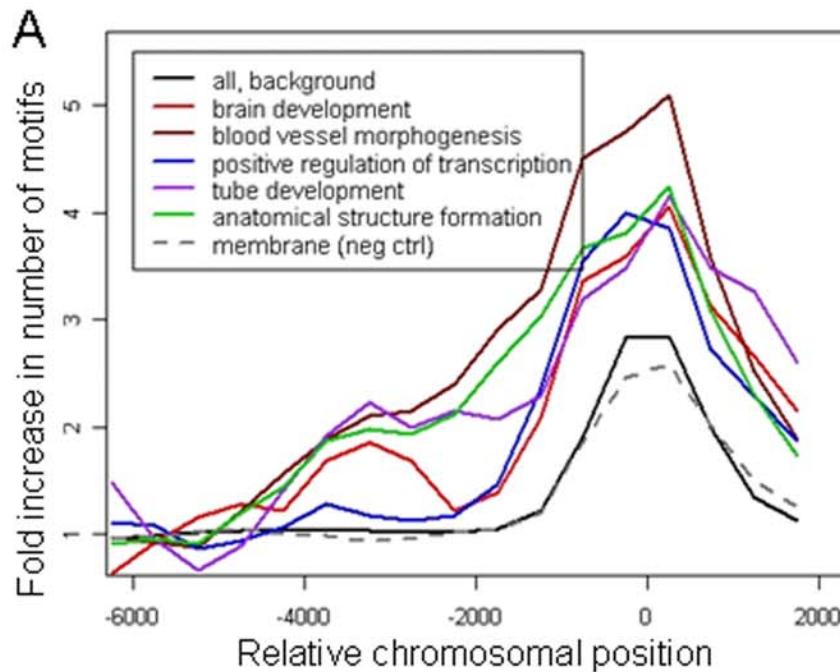
Supplemental Material Figure 2

Supplemental Material Figure 3. Ingenuity Pathway Analysis. The top scoring interaction network (score = 50) was obtained from the top 750 ranked genes in wild type naïve cells for the comparison of anti-AHR immunoprecipitation with the IgG control. Note the prominent role of regulatory interactions with the WNT pathway.



Supplemental Material Fig. 3

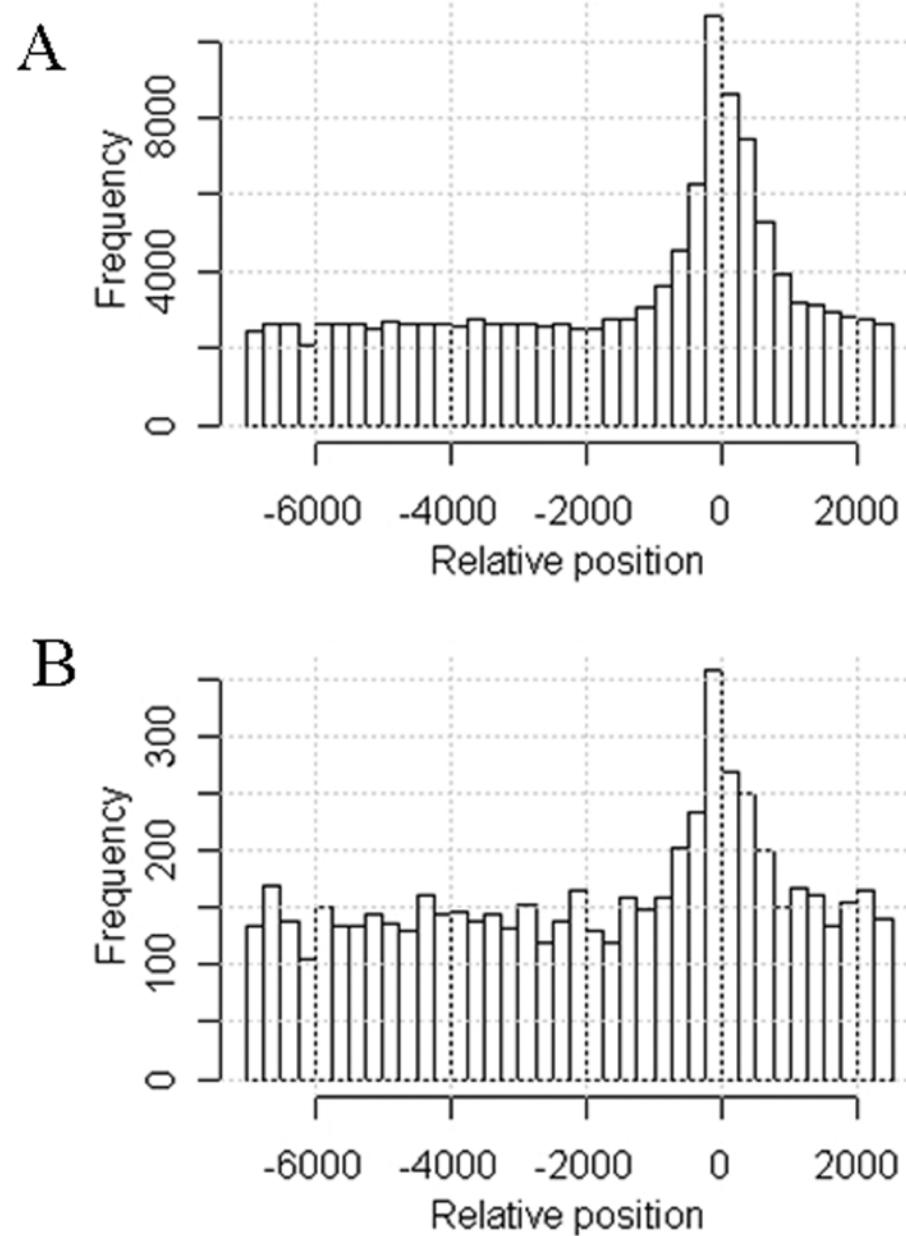
Supplemental Material Figure 4. Enrichment of AHR binding motifs in the genes identified by ChIP/chip. The relative position in gene promoters of AHR binding motifs was determined for the indicated biological processes, and fold increase over baseline, as defined by the sequence upstream of -4kb, was calculated. **(A)** Genes identified by ChIP/chip and belonging to the selected sets of biological processes from Figure 4 show an enrichment of AHR binding motifs over baseline compared with that in all genes, whereas genes belonging to a non-enriched GO term did not show the same level of enrichment. **(B)** Genes not identified by ChIP/chip but still belonging to one of the same biological processes showed little to no signal compared with that in all genes. **(C)** Enrichment in genes belonging to any of the top 10 enriched biological processes based on ChIP/chip data alone is shown for (i) genes identified by ChIP/chip, (ii) genes not identified by ChIP/chip, and (iii) all genes.



Supplemental Material Fig. 4

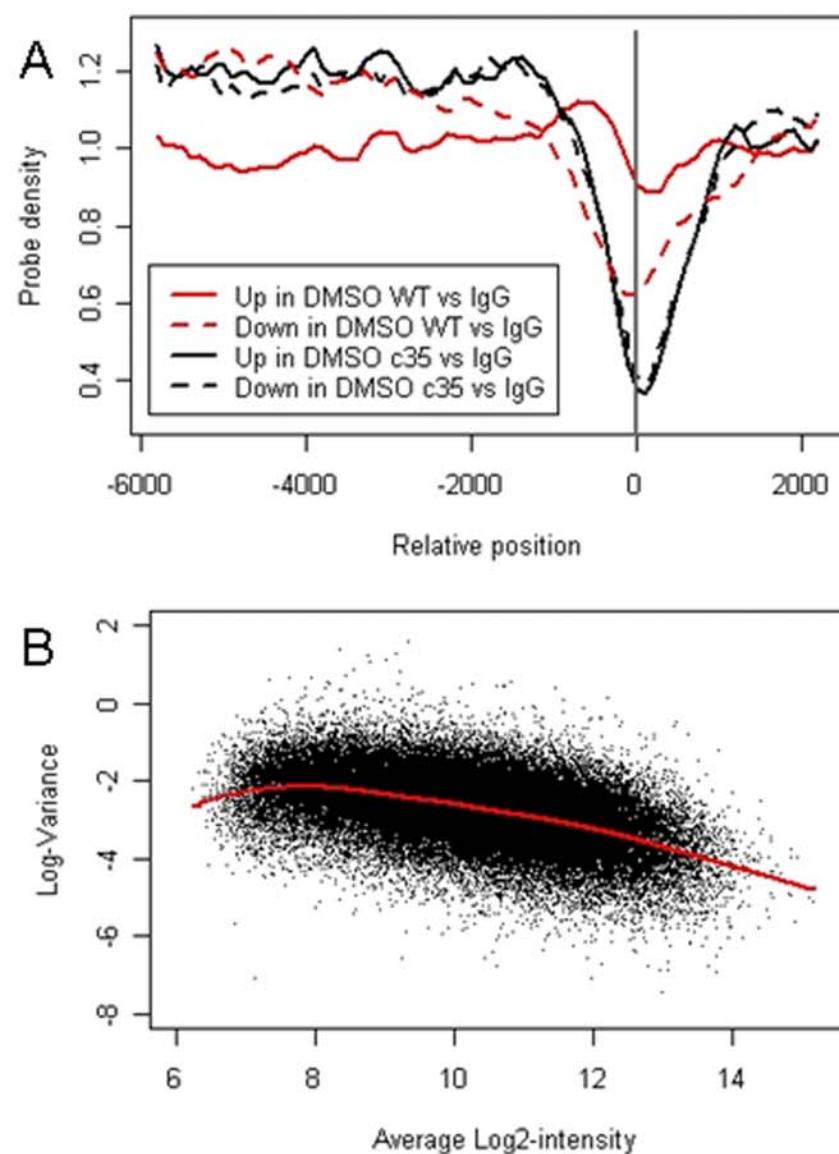
Supplemental Material Figure 5. Analysis of AHR binding motif position.

We determined the relative positions in gene promoters of two AHR binding motifs, the canonical 5-nucleotide motif 5'-GCGTG-3' and the longer 18 base-pair motif 5'-CCYCNRRSTNGCGTGASA-3', defined by the TRANSFAC Position Weight Matrix V\$AHR_01. Both motifs showed the same relative signal position, but of the two motifs, the shorter (**A**) gave a higher peak signal-to-noise ratio (approximately 4.5 fold-ratio compared to 3) than the longer (**B**).



Supplemental Material Figure 5

Supplemental Material Figure 6. ChIP/chip analysis workflow. **(A)** The histogram shows the chromosomal location of probes with high fold changes in control DMSO treated cells immunoprecipitated with anti-AHR compared to control IgG (ratio>1.5-fold). Solid lines indicate probes that have higher binding in naïve cell IP'd with anti-AHR than IgG. In naïve wild type cells there are more high-fold upward changes near the start sites for anti-AHR than for IgG, as expected. This is not observed for c35 cells. Dotted lines indicate higher binding for IgG immunoprecipitation than for anti-AHR, and this is expected to be flat for both wild type and c35 cells. **(B)** Relationship between probe variance and signal level, showing approximately 8-fold difference in variance along entire range in signal. The result shown in this figure, together with Supplemental Material Figure 1A, explains the unintuitive results of **(A)** above as an artifact of higher variance levels for probes residing farther from the TSS of a gene.



Supplemental Material Figure 6